

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds
(without alignments)
71.766 Million cell updates/sec

Title: US-09-787-443A-20

Perfect score: 11

Sequence: 1 AKKKEQKQRNA 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	11	100.0	11	3	AAY88548	Aay88548 NCAM Ig1
2	11	100.0	11	5	ABG69348	Abg69348 Human neu
3	4	36.4	11	2	AAR55163	Aar55163 Fragment
4	4	36.4	11	2	AAR85318	Aar85318 Human ret
5	4	36.4	11	2	AAW24438	Aaw24438 Nucleic a
6	4	36.4	11	3	AAY51589	Aay51589 HIV-1 der
7	4	36.4	11	3	AAY88558	Aay88558 NCAM Ig1
8	4	36.4	11	4	AAB50076	Aab50076 csk tyros
9	4	36.4	11	4	AAB99418	Aab99418 Staphylok

10	4	36.4	11	4	AAE08102	Aae08102 Peptide #
11	4	36.4	11	5	ABB74590	Abb74590 Transcrip
12	4	36.4	11	5	ABB74327	Abb74327 Bipartite
13	4	36.4	11	5	ABB74509	Abb74509 DNA repai
14	4	36.4	11	5	AAO18012	Aao18012 Human imm
15	3	27.3	11	2	AAR07649	Aar07649 t-PA spec
16	3	27.3	11	2	AAR08092	Aar08092 Antifreez
17	3	27.3	11	2	AAR31360	Aar31360 Antimicro
18	3	27.3	11	2	AAR24793	Aar24793 Sequence
19	3	27.3	11	2	AAR35381	Aar35381 Amphiphil
20	3	27.3	11	2	AAR43429	Aar43429 Ro/SSA ep
21	3	27.3	11	2	AAR33973	Aar33973 Amphiphil
22	3	27.3	11	2	AAR31163	Aar31163 C-termina
23	3	27.3	11	2	AAR34255	Aar34255 Mutant HT
24	3	27.3	11	2	AAR34248	Aar34248 Mutant HT
25	3	27.3	11	2	AAR41495	Aar41495 TNF inhib
26	3	27.3	11	2	AAR31493	Aar31493 P3 OF 31-
27	3	27.3	11	2	AAR35026	Aar35026 GMP-140 M
28	3	27.3	11	2	AAR45132	Aar45132 Amphiphil
29	3	27.3	11	2	AAR60841	Aar60841 Polyoxime
30	3	27.3	11	2	AAR50563	Aar50563 Amphiphil
31	3	27.3	11	2	AAR55987	Aar55987 Ion chann
32	3	27.3	11	2	AAR59065	Aar59065 Cancer tr
33	3	27.3	11	2	AAR56948	Aar56948 Peptide w
34	3	27.3	11	2	AAR59984	Aar59984 Myc-tag p
35	3	27.3	11	2	AAR50448	Aar50448 Amphiphil
36	3	27.3	11	2	AAR72301	Aar72301 Anti-HIV
37	3	27.3	11	2	AAR72299	Aar72299 Anti-HIV
38	3	27.3	11	2	AAR68911	Aar68911 Factor-VI
39	3	27.3	11	2	AAR66766	Aar66766 Zinc-fing
40	3	27.3	11	2	AAR84083	Aar84083 Human lac
41	3	27.3	11	2	AAR67858	Aar67858 FVII/TF m
42	3	27.3	11	2	AAW21466	Aaw21466 Islet amy
43	3	27.3	11	2	AAW21220	Aaw21220 Farnesyl
44	3	27.3	11	2	AAW21471	Aaw21471 Collagena
45	3	27.3	11	2	AAR76917	Aar76917 Thymosin
46	3	27.3	11	2	AAR79718	Aar79718 Optimal p
47	3	27.3	11	2	AAR90267	Aar90267 Ion-chann
48	3	27.3	11	2	AAR90259	Aar90259 Ion-chann
49	3	27.3	11	2	AAR91788	Aar91788 Ion-chann
50	3	27.3	11	2	AAR91787	Aar91787 Ion-chann
51	3	27.3	11	2	AAR76755	Aar76755 E. coli F
52	3	27.3	11	2	AAR66819	Aar66819 Mouse syn
53	3	27.3	11	2	AAR98139	Aar98139 C-myc epi
54	3	27.3	11	2	AAW09326	Aaw09326 Myc epitope
55	3	27.3	11	2	AAW04041	Aaw04041 Antifunga
56	3	27.3	11	2	AAR92030	Aar92030 Hydrophil
57	3	27.3	11	2	AAW01038	Aaw01038 Myc epitope
58	3	27.3	11	2	AAW11753	Aaw11753 T-cell re
59	3	27.3	11	2	AAW12383	Aaw12383 Myc.1 epi
60	3	27.3	11	2	AAW18499	Aaw18499 Amino-ter
61	3	27.3	11	2	AAW21913	Aaw21913 Smooth mu
62	3	27.3	11	2	AAW09909	Aaw09909 Prostate
63	3	27.3	11	2	AAW44580	Aaw44580 Anti-fung
64	3	27.3	11	2	AAW38865	Aaw38865 Delivery
65	3	27.3	11	2	AAW38785	Aaw38785 Delivery
66	3	27.3	11	2	AAW38822	Aaw38822 Delivery

67	3	27.3	11	2	AAW26074	Aaw26074 M32 deriv
68	3	27.3	11	2	AAW16616	Aaw16616 Phosphoin
69	3	27.3	11	2	AAW19819	Aaw19819 Universal
70	3	27.3	11	2	AAW43762	Aaw43762 Bacterici
71	3	27.3	11	2	AAW26548	Aaw26548 Epithelia
72	3	27.3	11	2	AAW76269	Aaw76269 Human cal
73	3	27.3	11	2	AAW50917	Aaw50917 Amino aci
74	3	27.3	11	2	AAW65554	Aaw65554 Multiply
75	3	27.3	11	2	AAW61490	Aaw61490 Nuclear 1
76	3	27.3	11	2	AAW62116	Aaw62116 Human MDM
77	3	27.3	11	2	AAW66523	Aaw66523 Amphiphil
78	3	27.3	11	2	AAW53153	Aaw53153 PTP activ
79	3	27.3	11	2	AAW56038	Aaw56038 Chimeric
80	3	27.3	11	2	AAW50245	Aaw50245 C-myc tag
81	3	27.3	11	2	AAW61607	Aaw61607 c-myc mon
82	3	27.3	11	2	AAW54579	Aaw54579 Peptide 2
83	3	27.3	11	2	AAW76757	Aaw76757 Murine si
84	3	27.3	11	2	AAW44012	Aaw44012 Human c-m
85	3	27.3	11	2	AAW51429	Aaw51429 Nuclear 1
86	3	27.3	11	2	AAW82585	Aaw82585 Seq ID 20
87	3	27.3	11	2	AAY67197	Aay67197 Spacer mo
88	3	27.3	11	2	AAW86735	Aaw86735 Anticoagu
89	3	27.3	11	2	AAY45432	Aay45432 Immunogen
90	3	27.3	11	2	AAW99810	Aaw99810 c-myc epi
91	3	27.3	11	2	AAY17757	Aay17757 Myc epitope
92	3	27.3	11	2	AAW92490	Aaw92490 SV40 T-an
93	3	27.3	11	2	AAW77457	Aaw77457 Lipophilic
94	3	27.3	11	2	AAM52998	Aam52998 Antifunga
95	3	27.3	11	2	AAV00557	Aay00557 Antifunga
96	3	27.3	11	2	AAV27327	Aay27327 A tag pep
97	3	27.3	11	2	AAW81004	Aaw81004 S. cerevisiae
98	3	27.3	11	2	AAV15395	Aay15395 Peptide 1
99	3	27.3	11	2	AAV10761	Aay10761 Peptide u
100	3	27.3	11	2	AAV10750	Aay10750 Peptide u

ALIGNMENTS

RESULT 1
 AAY88548
 ID AAY88548 standard; peptide; 11 AA.
 XX
 AC AAY88548;
 XX
 DT 07-AUG-2000 (first entry)
 XX
 DE NCAM Ig1 binding peptide #20.
 XX
 KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 KW treatment; prosthetic nerve guide; treatment; nervous system.
 XX
 OS Synthetic.
 XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.

XX

PS Example 4; Page 25; 119pp; English.

XX

CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject

XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKKEQKQRNA 11

|||||||

Db 1 AKKKEQKQRNA 11

RESULT 2

ABG69348

ID ABG69348 standard; peptide; 11 AA.

XX

AC ABG69348;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #20.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,
PT in the preparation of medicament for preventing death of cells presenting
PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which
CC comprises at least 5 contiguous amino acid residues of a sequence of the
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,
CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
CC of a medicament for preventing death of cells presenting the NCAM or an
CC NCAM ligand. The medicament is for the stimulation of the survival of
CC heart muscle cells, such as survival after acute myocardial infarction.
CC The medicament is for the treatment of diseases or conditions of the
CC central and peripheral nervous system, such as postoperative nerve
CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
CC impaired myelination of nerve fibres, postischaemic damage, e.g.
CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
CC degeneration associated with diabetes mellitus, neuro-muscular
CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
CC Huntington's disease. The medicament is for the treatment of diseases or
CC conditions of the muscles including conditions with impaired function of
CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
CC disorders, and for the treatment of diseases of conditions of various
CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
CC ABG69352 represent human NCAM peptides of the invention

XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AKKKEQKQRNA 11
Db	1 AKKKEQKQRNA 11

RESULT 3
AAR55163
ID AAR55163 standard; protein; 11 AA.
XX
AC AAR55163;
XX
DT 25-MAR-2003 (revised)
DT 11-JAN-1995 (first entry)
XX
DE Fragment of retinoic acid receptor RAR-beta.
XX
KW Liver; hap; retinoic acid receptor; steroid; thyroid; hormone; hepatoma;
KW retinoid; antibody.
XX
OS Homo sapiens.
XX
PN US5317090-A.
XX
PD 31-MAY-1994.
XX
PF 11-DEC-1992; 92US-00989902.
XX
PR 16-DEC-1987; 87US-00133687.
PR 17-DEC-1987; 87US-00134130.
PR 20-JUN-1988; 88US-00209009.
PR 30-NOV-1988; 88US-00278136.
PR 30-MAR-1989; 89US-00330405.

PR 21-AUG-1991; 91US-00751612.
PR 30-MAR-1992; 92US-00860577.
XX
PA (INSP) INST PASTEUR.
XX
PI Marchio A, Chambon P, Petkovich M, Krust A, Dejean A, Tiollais P;
PI Brand N, De The HB;
XX
DR WPI; 1994-176333/21.
XX
PT Antibody specific for retinoic acid receptor-beta - useful for detecting,
PT quantifying and identifying agonists and antagonists of retinoid
PT activity.
XX
PS Claim 4; Col 40; 35pp; English.
XX
CC The retinoic acid receptor RAR-beta is encoded by a gene designated hap.
CC The hap gene is transcribed at low level in most human tissues, but the
CC gene is overexpressed in prostate and kidney. Six out of seven hepatoma or
CC hepatoma-derived cell lines express a small hap transcript which is
CC undetectable in normal adult and foetal livers but present in all non-
CC hepatic tissues tested. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKKE 5
 ||||
Db 6 KKKE 9

RESULT 4
AAR85318
ID AAR85318 standard; peptide; 11 AA.
XX
AC AAR85318;
XX
DT 25-MAR-2003 (revised)
DT 19-AUG-1996 (first entry)
XX
DE Human retinoic acid receptor RAR-beta (human liver HAP) peptide-2.
XX
KW HAP; liver; hepatoma; retinoic acid receptor; RAR-beta; psoriasis;
KW atherosclerosis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US5468617-A.
XX
PD 21-NOV-1995.
XX
PF 02-FEB-1994; 94US-00190555.
XX
PR 16-DEC-1987; 87US-00133687.

PR 17-DEC-1987; 87US-00134130.
PR 20-JUN-1988; 88US-00209009.
PR 30-NOV-1988; 88US-00278136.
PR 30-MAR-1989; 89US-00330405.
PR 21-AUG-1991; 91US-00751612.
PR 30-MAR-1992; 92US-00860577.
PR 11-DEC-1992; 92US-00989902.
PR 22-JUL-1993; 93US-00095706.

XX

PA (TIOL/) TIOLLAIS P.
PA (DEJE/) DEJEAN A.
PA (KRUS/) KRUST A.
PA (PETK/) PETKOVICH M.
PA (DTHE/) BLAUDIN DE THE H.
PA (MARC/) MARCHIO A.
PA (BRAN/) BRAND N.
PA (CHAM/) CHAMBON P.

XX

PI Brand N, Chambon P, Blaudin De The H, Marchio A, Dejean A;
PI Petkovich M, Krust A, Tiollais P;

XX

DR WPI; 1996-010094/01.

XX

PT Method for screening for retinoic acid receptor-beta (ant)agonists -
PT useful for blood testing and for treatment of rheumatoid arthritis,
PT psoriasis, atherosclerosis etc.

XX

PS Claim 7; Col 39-40; 35pp; English.

XX

CC This RAR-beta peptide-2 fragment is part of a protein which may be
CC expressed recombinantly in bacterial host cells such as Escherichia coli
CC TG-1. The protein, which is free from human, blood-derived protein, forms
CC a complex with an agonist or antagonist. The protein may be used in a
CC novel method for assaying a fluid for the presence of an agonist or
CC antagonist to retinoic acid receptor, RAR-beta. (Updated on 25-MAR-2003
CC to correct PF field.)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKKE 5
 ||||
Db 6 KKKE 9

RESULT 5

AAW24438

ID AAW24438 standard; peptide; 11 AA.

XX

AC AAW24438;

XX

DT 30-SEP-1997 (first entry)

XX

DE Nucleic acid (NA) binding peptide used in NA delivery to cells.

XX
KW Nucleic acid transporter; gene therapy; binding complex; lysis agent;
KW JTS-1; K8; alpha helix; endosome; lysosome; nucleus targeting.
XX
OS Synthetic.
XX
PN WO9640958-A1.
XX
PD 19-DEC-1996.
XX
PF 23-APR-1996; 96WO-US005679.
XX
PR 07-JUN-1995; 95US-00484777.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Smith LC, Sparrow JT, Woo SL;
XX
DR WPI; 1997-052345/05.
XX
PT Nucleic acid transporter useful in gene therapy - contains binding
PT complex associated with surface and nuclear ligands and lysis agent.
XX
PS Disclosure; Page 49; 125pp; English.
XX
CC AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both
CC condensing and stabilising a NA. The peptides can be conjugated to a
CC lytic peptide to form a nucleic acid transporter system. The lysis agent
CC forms an alpha-helical structure. The transporter system is used to
CC deliver nucleic acid to a cell and for treating humans by gene therapy.
CC By taking advantage of the characteristics of both the lysis agents and
CC the binding molecules, delivery of the nucleic acid is enhanced. Specific
CC lysis agents are capable of releasing the nucleic acid into the cellular
CC interior from the endosome. Release is efficient without
CC endosomal/lysosomal degradation. Once released the binding complexes help
CC target the nucleic acid to the nucleus
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKK 4
|||
Db 3 AKKK 6

RESULT 6
AAY51589
ID AAY51589 standard; peptide; 11 AA.
XX
AC AAY51589;
XX
DT 12-SEP-2003 (revised)
DT 25-MAY-2000 (first entry)
XX

DE HIV-1 derived GP120 peptide fragment #1.
XX
KW Plastic carrier surface; detection; gp120.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200005584-A1.
XX
PD 03-FEB-2000.
XX
PF 21-JUL-1999; 99WO-NL000470.
XX
PR 21-JUL-1998; 98NL-01009703.
XX
PA (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
XX
PI Puijk WC;
XX
DR WPI; 2000-182757/16.
XX
PT Ultra flat plastic carrier surfaces by molding on to smooth non-adhesive
PT surfaces, e.g. mica or glass, and release, can carry active groups for
PT coupling to analytes, also form submicrotiter size wells suitable for
PT microprinting techniques.
XX
PS Disclosure; Fig 9; 47pp; English.
XX
CC This invention describes a novel method for the manufacture of an ultra
CC flat plastic carrier surface, by laying on to a very smooth auxiliary
CC surface, treating the plastic so that the surface roughness of the side
CC facing the auxiliary is reduced, and removal; coupling of chemical and
CC biochemical analytes for examination through active groups on the plastic
CC surface; surface of plastic suitable for microjet printing techniques.
CC Examples of applications of the surface include investigations of
CC biological materials; peptides, proteins, saccharides, cells, viruses,
CC antigens, and information carrying polymers, i.e. DNA or RNA, or their
CC fragments, all optionally attached via linkers. Detection and
CC determination of materials of interest can be carried out as in standard
CC practice, e.g., ELISA, fluorescence, color, or radiation, except that
CC very small amounts may be assayed or investigated. Conveniently, the
CC surface can be as a matrix of microwells for these purposes; these can be
CC molded into the surface by having hemispheres on the forming surface. The
CC plastic surface is so smooth that it can bind very small amounts of
CC materials of interest, which can be detected perfectly, even when close
CC together on the surface by microscopy and/or photography, e.g., a
CC confocal scanner, without interference from humps and hollows causing bad
CC focussing. AAY51589-Y51596 represent peptide fragments derived from the
CC human immunodeficiency virus type 1 gp120 protein which are used to
CC illustrate the method of the invention. (Updated on 12-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEQK 7
|||
Db 1 KEQK 4

RESULT 7

AAY88558

ID AAY88558 standard; peptide; 11 AA.

XX

AC AAY88558;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Ig1 binding peptide 121 used as a control peptide.

XX

KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.

XX

PD 06-APR-2000.

XX

PF 23-SEP-1999; 99WO-DK000500.

XX

PR 29-SEP-1998; 98DK-00001232.

PR 29-APR-1999; 99DK-00000592.

XX

PA (RONN/) RONN L C B.

PA (BOCK/) BOCK E.

PA (HOLM/) HOLM A.

PA (OLSE/) OLSEN M.

PA (OSTE/) OSTERGAARD S.

PA (JENS/) JENSEN P H.

PA (POUL/) POULSEN F M.

PA (SORO/) SOROKA V.

PA (RALE/) RALETS I.

PA (BERE/) BEREZIN V.

XX

PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX

DR WPI; 2000-293111/25.

XX

PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.

XX

PS Example 5; Fig 7; 119pp; English.

XX

CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.

CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three

CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The invention relates to a compound containing a peptide which
CC binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2 domains,
CC and is capable of stimulating or promoting neurite outgrowth from NCAM
CC presenting cells, and is also capable of promoting the proliferation of
CC NCAM presenting cells. The present sequence represents a control peptide
CC used in the identification of those binding peptides which can be used in
CC the compound. The compound may be used in the treatment of normal,
CC degenerated or damaged NCAM presenting cells. The compound may in
CC particular be used to treat diseases of the central and peripheral
CC nervous systems such as post operative nerve damage, traumatic nerve
CC damage, impaired myelination of nerve fibres, conditions resulting from a
CC stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis,
CC nerve degeneration associated with diabetes mellitus, disorders affecting
CC the circadian clock or neuro-muscular transmission and schizophrenia.
CC Conditions affecting the muscles may also be treated with the compound,
CC such as conditions associated with impaired function of neuromuscular
CC connections (e.g. genetic or traumatic shock or traumatic atrophic muscle
CC disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus
CC types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also
CC be treated using the compound. The compound is used in a prosthetic nerve
CC guide, and also to stimulate the ability to learn, and to stimulate the
CC memory of a subject

XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKK 4
 ||||
Db 1 AKKK 4

RESULT 8
AAB50076
ID AAB50076 standard; peptide; 11 AA.
XX
AC AAB50076;
XX
DT 19-MAR-2001 (first entry)
XX
DE csk tyrosine kinase substrate.
XX
KW MLSK; MDCK; autoimmune disorder; Large NIK-Related Kinase 1;
KW wound healing; periodontal disease; inflammatory disease; tumour;
KW infection; allergy; LNRK1.
XX
OS Unidentified.
XX
PN WO200073468-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014696.

XX
PR 28-MAY-1999; 99US-0136781P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Bird TA, Virca GD, Martin U, Anderson DM;
XX
DR WPI; 2001-061546/07.
XX
PT Novel murine and human kinase nucleic acids useful for treating
PT inflammations, infections, tumors, allergies, autoimmune diseases, and
PT for stimulating or suppressing immune responses.
XX
PS Example 5; Page 70; 106pp; English.
XX
CC The present invention relates to kinases (MDCK-1, -2 and -3 and MLSK-1
CC and -2; see AAB50053-B50057, and LNRK-1; see AAB50059). The kinases of
CC the present invention are useful for treating a variety of disorders
CC listed in the disclosure of the specification, including autoimmune
CC disorders, allergic reactions, myeloid or lymphoid cell deficiencies,
CC wound healing and tissue repair and replacement, burns, incisions and
CC ulcers, periodontal disease, inflammatory diseases, tumours and
CC bacterial, viral or fungal infection. The present sequence is a peptide
CC kinase substrate used in the present invention to investigate the
CC substrate specificity of MLSK-1
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKKE 5
Db 2 KKKE 5

RESULT 9
AAB99418
ID AAB99418 standard; peptide; 11 AA.
XX
AC AAB99418;
XX
DT 28-AUG-2001 (first entry)
XX
DE Staphylokinase T-cell epitope 90-100.
XX
KW Staphylokinase; Staphylococcus aureus; SakSTAR; T-cell epitope;
KW immunogenic; thrombolytic; acute myocardial infarction; immunogenicity.
XX
OS Staphylococcus aureus.
XX
PN WO200140281-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-EP012299.

XX
PR 02-DEC-1999; 99EP-00204093.
XX
PA (THRO-) THROMB-X NV.
XX
PI Warmerdam PAM, Plaisance SDNGH, Collen DJ, De Maeyer MCH;
XX
DR WPI; 2001-374786/39.
XX
PT Reducing immunogenicity of protein (P) by eliminating T cell epitopes in
PT test peptides having amino acid sequence corresponding to (P) and
PT modifying amino acid sequence of (P) according to test peptide
PT modifications.
XX
PS Example 4; Page 19; 50pp; English.
XX
CC The present invention describes a method for reducing the immunogenicity
CC of a peptide or protein (I), where (I) can be staphylokinase (SakSTAR)
CC isolated from *Staphylococcus aureus*. The method involves designing a
CC series of overlapping test peptides having an amino acid sequence
CC corresponding to (I), modifying test peptides which are identified to
CC comprise one or more T-cell epitopes, such that they are reduced or
CC eliminated, and repeating the T-cell eliminating modifications for (I) to
CC produce a modified peptide or protein. Methods from the present invention
CC can be used for the treatment, diagnosis or prophylaxis or for the
CC preparation of a pharmaceutical composition for the treatment, diagnosis
CC or prophylaxis of a human subject. Staphylokinase is used as a potent
CC thrombolytic agent in patients with acute myocardial infarction. The
CC method is useful for reducing cell based immunogenicity of non-human
CC proteins such as streptokinase or antibodies or their fragments, from
CC other species, for diagnostics and treatment of human disease. AAB99400
CC to AAB99449 represent amino acid sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKKE 5
 ||||
Db 7 KKKE 10

RESULT 10
AAE08102
ID AAE08102 standard; peptide; 11 AA.
XX
AC AAE08102;
XX
DT 01-NOV-2001 (first entry)
XX
DE Peptide #1 from human ribonucleoprotein, 60 kD Ro/SSA.
XX
KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.

XX
OS Homo sapiens.
XX
PN US6232522-B1.
XX
PD 15-MAY-2001.
XX
PF 30-NOV-1993; 93US-00160604.
XX
PR 31-JAN-1990; 90US-00472947.
PR 31-JAN-1991; 91US-00648205.
PR 13-APR-1992; 92US-00867819.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI Harley JB, James JA, Scofield RH;
XX
DR WPI; 2001-335087/35.
XX
PT Generating systemic lupus erythematosus animal model by immunizing non-
PT human animal with non-immunoglobulin peptide having amino acid sequence
PT of self-antigen bound by autoantibody population in early stage of
PT disease.
XX
PS Claim 10; Col 100; 63pp; English.
XX
CC The patent discloses a specific method of generating an animal model of
CC systemic lupus erythematosus (SLE), comprising immunising a non- human
CC animal with non-immunoglobulin peptide which comprises an epitope
CC immunoreactive with auto-antibody (AAb) from patient with SLE. The
CC epitope includes a region of self-antigen which is bound by AAb
CC population present in early stage in patient with SLE. The method is used
CC for generating an animal model of SLE. It is useful for screening
CC therapeutics effective in treating autoimmune disorders. It is useful as
CC a component in a diagnostic assay, as a therapeutic (vaccine to block the
CC AAbs produced, by eliciting immune response), and in research on the
CC possible causes of the autoimmune diseases. The method is used to
CC interrupt the course of an autoimmune response, once autoimmunity against
CC the autoantigen is established. The amino acid sequences are used to make
CC agents for neutralising circulating antibodies or immobilised on
CC substrates in extracorporeal devices for specific removal of AAbs. The
CC reagents identified by using the method are useful in manufacturing and
CC testing autoantigens. The method is useful as models for screening of
CC compounds which induce autoimmunity, inhibit induction of autoimmunity,
CC suppress autoimmunity. It is useful in diagnosis of autoimmunity and as
CC therapeutics for the treatment of autoimmune disorders. The present
CC sequence is a peptide from human ribo- nucleoprotein, 60 kD Ro/SSA. This
CC peptide is used in the exemplification of the invention.
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEQK 7
||||

RESULT 11

ABB74590

ID ABB74590 standard; peptide; 11 AA.

XX

AC ABB74590;

XX

DT 18-APR-2002 (first entry)

XX

DE Transcription factor nuclear localisation signal peptide SEQ ID NO:354.

XX

KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.

XX

OS Homo sapiens.

XX

PN WO200193836-A2.

XX

PD 13-DEC-2001.

XX

PF 08-JUN-2001; 2001WO-US018657.

XX

PR 09-JUN-2000; 2000US-0210925P.

XX

PA (BOUL/) BOULIKAS T.

XX

PI Boulikas T;

XX

DR WPI; 2002-164295/21.

XX

PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.

XX

PS Claim 14; Page 76; 107pp; English.

XX

CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated

CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKKE 5
|||
Db 6 KKKE 9

RESULT 12

ABB74327

ID ABB74327 standard; peptide; 11 AA.

XX

AC ABB74327;

XX

DT 18-APR-2002 (first entry)

XX

DE Bipartite/split nuclear localisation signal peptide SEQ ID NO:91.

XX

KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.

XX

OS Synthetic.

XX

PN WO200193836-A2.

XX

PD 13-DEC-2001.

XX

PF 08-JUN-2001; 2001WO-US018657.

XX

PR 09-JUN-2000; 2000US-0210925P.

XX

PA (BOUL/) BOULIKAS T.

XX

PI Boulikas T;

XX

DR WPI; 2002-164295/21.

XX

PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.

XX

PS Claim 14; Page 58; 107pp; English.

XX

CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on

CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKK 4
 ||||
Db 7 AKKK 10

RESULT 13

ABB74509

ID ABB74509 standard; peptide; 11 AA.

XX

AC ABB74509;

XX

DT 18-APR-2002 (first entry)

XX

DE DNA repair protein nuclear localisation signal peptide SEQ ID NO:273.

XX

KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.

XX

OS Drosophila sp.

XX

PN WO200193836-A2.

XX

PD 13-DEC-2001.

XX

PF 08-JUN-2001; 2001WO-US018657.

XX

PR 09-JUN-2000; 2000US-0210925P.

XX

PA (BOUL/) BOULIKAS T.

XX

PI Boulikas T;

XX
DR WPI; 2002-164295/21.
XX
PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.
XX
PS Claim 14; Page 71; 107pp; English.
XX
CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5
|||
Db 6 KKKE 9

RESULT 14
AAO18012
ID AAO18012 standard; peptide; 11 AA.
XX
AC AAO18012;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human immunoglobulin E epitope SEQ ID NO: 4.
XX
KW Allergy; immunoglobulin E; IgE; vaccine; immunogen; epitope; human;
KW non-anaphylactogenic; antiallergic.
XX
OS Homo sapiens.
XX

PN WO200234288-A2.
XX
PD 02-MAY-2002.
XX
PF 24-OCT-2001; 2001WO-EP012392.
XX
PR 27-OCT-2000; 2000GB-00026334.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Vinals Y De BassolsC;
XX
DR WPI; 2002-479702/51.
XX
PT New peptides epitopes and mimotopes derived from IgE, useful for treating
PT or preventing allergies, for typing circulating anti-IgE, or for
PT diagnosing atopy.
XX
PS Claim 1; Page 4; 28pp; English.
XX
CC The present invention provides peptide epitopes derived from human
CC immunoglobulin E (IgE), which are non-anaphylactogenic and can be used as
CC immunogens to diagnose and treat allergies. The present sequence is an
CC epitope of the invention
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 KQRN 10
Db 3 KQRN 6

RESULT 15
AAR07649
ID AAR07649 standard; peptide; 11 AA.
XX
AC AAR07649;
XX
DT 25-MAR-2003 (revised)
DT 31-JAN-1991 (first entry)
XX
DE t-PA specific binding epitope.
XX
KW Tissue plasminogen activator; t-PA; immunogen catalase; assay; diagnosis;
KW monoclonal antibody; binding epitope.
XX
OS Synthetic.
XX
PN EP392369-A.
XX
PD 17-OCT-1990.
XX
PF 05-APR-1990; 90EP-00106568.

XX
PR 11-APR-1989; 89DE-03911794.
XX
PA (THOM) THOMAE GMBH KARL.
XX
PI Werner RG, Berthold W, Werz W, Jung G, Gombert F;
XX
DR WPI; 1990-314091/42.
XX
PT New monoclonal antibodies against tissue plasminogen activator - with
PT defined epitope specificity, useful for diagnosis, assay, purifcn. etc.
XX
PS Disclosure; Page 4; 17pp; German.
XX
CC MAb 17-134/11 was prep'd. using a conjugate of this peptide (amino acid
CC 343-354 of t-PA) with catalase as the immunogen. This antibody reacts
CC with both native and reduced carboxymethylated t-PA and peptide-scanning
CC showed that the min. sequence required for binding is EEEQK (347-351).
CC This binding is promoted by N-terminal VPG and C-terminal FEV sequences.
CC The Ab is useful analytically as diagnostic reagent, for purifying
CC recombinant human t-PA, for drug targetting and as therapeutic agent.
CC They can also be used to predict prim., sec. or tert. structures of t-PA;
CC to differentiate t-PA from other PAs and between various t-PA forms, and
CC to examine structure-function relationships of different t-PA regions.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 6 EQK 8

RESULT 16
AAR08092
ID AAR08092 standard; protein; 11 AA.
XX
AC AAR08092;
XX
DT 25-MAR-2003 (revised)
DT 01-MAR-1991 (first entry)
XX
DE Antifreeze segment #2 encoded by SS3.
XX
KW synthetic antifreeze polypeptide; cryopreservation;
KW core repetitive sequence.
XX
OS Synthetic.
XX
PN WO9013571-A.
XX
PD 15-NOV-1990.
XX

PF 10-MAY-1989; 89US-00350481.
XX
PR 10-MAY-1989; 89US-00350481.
PR 10-APR-1990; 90US-00507716.
XX
PA (DNAP) DNA PLANT TECHN COR.
XX
PI Warren GJ, Mueller JM, Mckown RJ, Dunsmuir P;
XX
DR WPI; 1990-361428/48.
XX
PT New anti-freeze poly-peptide(s) - used for cryo-protection of e.g. foods,
PT medically used biological(s), plant prods. or plants during growth.
XX
PS Disclosure; Fig 4; 11pp; English.
XX
CC Synthetic anti-freeze polypeptides (saf) comprise a specifically
CC cleavable site and a region containing at least two "core" segments such
CC as the 11mer given here. The saf's suppress ice crystal growth by binding
CC to the growing crystal face and blocking sites for further crystal
CC growth. They can be used to maximise retention of important properties of
CC organic materials through freezing and thawing processes. The basic
CC design of the polypeptides is based on known antifreeze polypeptides from
CC insects and fish, e.g. the winter flounder. See also AAQ06649-Q06652,
CC AAQ06656, AAQ06658, AAQ06660-Q06672, AAR08070-6, AAR08087-R08091,
CC AAR08093. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 8 AKK 10

RESULT 17
AAR31360
ID AAR31360 standard; peptide; 11 AA.
XX
AC AAR31360;
XX
DT 25-MAR-2003 (revised)
DT 20-MAY-1998 (first entry)
XX
DE Antimicrobial peptide #14 derived from bovine lactoferrin.
XX
KW antimicrobial agent; iron-binding protein; athlete's foot; mastitis;
KW antibacterial agent.
XX
OS Synthetic.
XX
PN EP503939-A1.

XX
PD 16-SEP-1992.
XX
PF 12-MAR-1992; 92EP-00302125.
XX
PR 13-MAR-1991; 91JP-00048196.
PR 24-APR-1991; 91JP-00094492.
PR 24-APR-1991; 91JP-00094493.
XX
PA (MORG) MORINAGA MILK IND CO LTD.
XX
PI Tomita M, Kawase K, Takase M, Bellamy WR, Yamauchi K;
PI Wakabayashi H, Tokita Y;
XX
DR WPI; 1992-310006/38.
XX
PT New antimicrobial peptide(s) - active against e.g. Listeria
PT monocytogenes, Staphylococcus aureus, Pseudomonas aeruginosa and
PT Klebsiella pneumoniae, for treating e.g. diarrhoea, mastitis, etc.
XX
PS Claim 8; Page 17; 19pp; English.
XX
CC This synthetic peptide has a sequence derived from bovine lactoferrin.
CC The peptide has stronger antimicrobial activity than unhydrolysed
CC lactoferrin and improved heat resistance. The peptide had a minimum
CC inhibitory concentration (microM) of 6, 12, 25 and 50 against Listeria
CC monocytogenes, Staphylococcus aureus, Pseudomonas aeruginosa and
CC Klebsiella pneumoniae, respectively. This and other peptides derived from
CC hydrolysed lactoferrin can be incorporated into foods, human or
CC veterinary compositions (e.g. for treating mastitis and athlete's foot),
CC toiletries, cosmetics, cleaning agents, etc. See AAR31350-R31361.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QRN 10
|||
Db 6 QRN 8

RESULT 18
AAR24793
ID AAR24793 standard; protein; 11 AA.
XX
AC AAR24793;
XX
DT 25-MAR-2003 (revised)
DT 02-JAN-1992 (first entry)
XX
DE Sequence of fibronectin-derived peptide which binds GPIIb-IIIa.
XX
KW Fibronectin; cell attachment; cell adhesion; adhesive glycoprotein.
XX

OS Homo sapiens.
XX
PN WO9209200-A1.
XX
PD 11-JUN-1992.
XX
PF 03-DEC-1991; 91WO-US009029.
XX
PR 03-DEC-1990; 90US-00620668.
PR 03-JUL-1991; 91US-00725600.
PR 27-NOV-1991; 91US-00803623.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Ginsberg MH, Plow EF, Bowditch R;
XX
DR WPI; 1992-216714/26.
XX
PT New polypeptide(s) derived from human fibronectin - promote cell
PT attachment to substrates, inhibit platelet aggregation and thrombus
PT formation and modulate coagulation and inflammatory response.
XX
PS Claim 4; Page 97; 112pp; English.
XX
CC AAQ25592 comprises bps 901-1506 of a human fibronectin (Fn)encoding DNA
CC sequence. It encodes AAs 1255-1456. The primary structure of Fn contains
CC three different types of internal repeats known as homology Types I,II
CC and III. A site contg. the Arg-Gly-Asp (RGD) sequence in the 10th Type
CC III repeat of Fn is known to be involved in cell adhesive events. The Fn
CC peptides of the invention bind to integrin receptors, particularly GPIIb-
CC IIIa, at a site which is independent of the RGD sequence. The new binding
CC site is located at least fifty AAs upstream of the RGD sequence (see
CC AAR24782). The claimed peptides are 100 AAs or less (see AAR24783-
CC R24796). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RNA 11
 |||
Db 7 RNA 9

RESULT 19
AAR35381
ID AAR35381 standard; peptide; 11 AA.
XX
AC AAR35381;
XX
DT 25-MAR-2003 (revised)
DT 07-JUN-1993 (first entry)
XX
DE Amphiphilic peptide #112 used to treat oral infections.
XX

KW Adverse oral conditions; amphipathic; anti-bacterial; anti-viral;
KW anti-fungal; dental plaque; dental caries; periodontal disease;
KW gingivitis; ionophore; ion-channel forming.
XX
OS Synthetic.
XX
PN WO9301723-A1.
XX
PD 04-FEB-1993.
XX
PF 09-JUL-1992; 92WO-US005757.
XX
PR 25-JUL-1991; 91US-00735070.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Berkowitz B, Jacob L;
XX
DR WPI; 1993-058434/07.
XX
PT Peptide(s) for prophylaxis and treatment of oral disorders - used for
PT periodontal disease, plaque, dental caries, gingivitis, etc.
XX
PS Claim 2; Page 129; 143pp; English.
XX
CC This is a specific example of a highly generic formula covering preferred
CC amphiphilic peptides for use in preventing or treating adverse oral
CC conditions. The peptide is an ionophore (i.e. an ion- channel forming
CC peptide) which has anti-bacterial, anti-viral, anti- fungal activity,
CC etc. making it suitable for use in oral compositions to treat or prevent
CC periodontal disease, plaque, dental caries, halitosis and gingivitis. The
CC anti-bacterial action will also be useful against bacteria associated
CC with dental implant infections and the peptides can stimulate the healing
CC of wounds in the oral cavity. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 20
AAR43429
ID AAR43429 standard; peptide; 11 AA.
XX
AC AAR43429;
XX
DT 25-MAR-2003 (revised)
DT 12-MAY-1994 (first entry)
XX
DE Ro/SSA epitope 44.

XX
KW Linear; epitope; 60 kD; Ro/SSA; La/SSB; autoantigen; E/F; G; 70 kD;
KW nuclear ribonucleoprotein; nRNP; Sm B/B'; polypeptide; antigen; D;
KW systemic lupus erythematosus; SLE; autoantibody; U4/U6; U5; B; B';
KW RNA polymerase III; U1; U2; Sjogrens syndrome; SS; human; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO9321223-A1.
XX
PD 28-OCT-1993.
XX
PF 13-APR-1993; 93WO-US003484.
XX
PR 13-APR-1992; 92US-00867819.
XX
PA (OKLA) UNIV OKLAHOMA STATE.
XX
PI Harley JB;
XX
DR WPI; 1993-351658/44.
XX
PT New linear epitope(s) for human auto-antibodies - from the Ro/SSA, La/SSB
PT and Sm B/B' antigens and ribo:nucleoprotein, used for diagnosing and
PT treating auto-immune disorders e.g. systemic lupus erythematosus.
XX
PS Claim 1; Page 30; 43pp; English.
XX
CC The sequences given in AAR43391-562 are linear epitopes which are derived
CC from the 60 kD Ro/SSA peptide, the La/SSB autoantigen, the 70 kD nuclear
CC ribonucleoprotein (nRNP) and the Sm B/B' polypeptide. These antigens are
CC common in systemic lupus erythematosus (SLE) and closely related
CC disorders. The Ro/SSA family of proteins has been shown to have several
CC molecular forms which are defined by the molecular weight of the antigen
CC identified. The major form has a molecular weight of 60 kD and two
CC additional forms have molecular weights of 52 and 54 kD. La/SSB is also a
CC member of this group of autoantibodies and binds small RNAs with a
CC polyuridine terminus. La/SSB is bound by a third of the anti-Ro/SSA
CC precipitin positive sera. La/SSB has been shown to be a 46-50 kD
CC monomeric phosphoprotein which associates with RNA polymerase III
CC transcripts. Anti-Sm antibodies precipitate snRNPs containing the U1, U2,
CC U4/U6 and U5 RNA. Anti-Sm antibodies may be directed against one or a
CC combination of the polypeptides: B (26 kD), B' (27 kD), D (13 kD), E/F
CC (11 kD doublet) and G (less than 10 kD). These epitopes may be used for
CC preventing, treating or screening autoimmune disorders, especially SLE or
CC Sjogrens syndrome (SS). They bind to a human autoantibody and may
CC therefore be used as vaccines. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEQ 6
|||

RESULT 21

AAR33973

ID AAR33973 standard; peptide; 11 AA.

XX

AC AAR33973;

XX

DT 25-MAR-2003 (revised)

DT 21-JUL-1993 (first entry)

XX

DE Amphiphilic peptide (e), #2.

XX

KW Hydrophobic; hydrophilic; neutral; (e); ionophore; channel-forming;
KW human; virus; antimicrobial; antiviral; antibacterial; antitumour;
KW antiparasitic; spermicide; preservative; sterilant; disinfectant;
KW wound healing; burn; infection; eye; cysts; spores; trophozoites; plants;
KW contamination.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "May be acetylated"

FT Modified-site 11

FT /note= "May be amidated"

XX

PN WO9305802-A1.

XX

PD 01-APR-1993.

XX

PF 04-SEP-1992; 92WO-US007622.

XX

PR 13-SEP-1991; 91US-00760054.

PR 20-APR-1992; 92US-00870960.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Maloy WL, Kari UP, Williams JI;

XX

DR WPI; 1993-117245/14.

XX

PT New biologically active amphiphilic peptide cpds. - having ion channel-forming properties used for inhibiting growth of target cells, virus or viral-infected cells.

XX

PS Claim 27; Page 33; 46pp; English.

XX

CC This sequence is an example of a biologically active peptide which
CC corresponds to the generic sequence; R1-R2-R2-R1-R1-R2-R2-R1-R2-R2-R1
CC where R1 = a hydrophobic amino acid; and R2 = a basic hydrophilic or
CC neutral hydrophilic amino acid. This basic structure was designated (e).
CC Peptides such as this are ionophores ie. they have channel-forming
CC properties. The peptides can be administered to a host, eg, humans, to
CC inhibit the growth of a target cell, virus or virally infected cell. They
CC can be used as antimicrobial, antiviral agents, antibacterial agents,

CC antitumour agents, antiparasitic agents, and as spermicides. They can be
CC used as preservatives or sterilants or disinfectants. These peptides can
CC also be used to promote or stimulate healing of wounds, to treat and/or
CC prevent prevent skin or burn infections, to prevent or treat eye
CC infections and to kill cysts, spores or trophozoites of infection causing
CC organisms. The peptides may also be administered to plants to prevent or
CC treat microbial, viral or parasitic contamination. (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 22

AAR31163

ID AAR31163 standard; peptide; 11 AA.

XX

AC AAR31163;

XX

DT 25-MAR-2003 (revised)

DT 10-MAY-1993 (first entry)

XX

DE C-terminal subst. amphiphilic peptide #112.

XX

KW ion-channel forming; ionophore; antibiotic; anti-tumour; anti-virus;
KW wound healing.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "Leu-(C=O)-T, T= O-R, NH-NH2, NH-OH or NR'R''; R= opt.substd. 1-10C aliphatic, aromatic or aralkyl gp.; R'', R''= H or from one of gps. i and ii; gp.i= 1-10C hydroxy-substd. aliphatic, aromatic or aralkyl gp.; gp.ii= amino-substd. aliphatic, aromatic, aralkyl or alkylaromatic gp. and at least one of R' and R'' = gp.i or gp.ii'"

XX

PN WO9222317-A1.

XX

PD 23-DEC-1992.

XX

PF 01-JUN-1992; 92WO-US004603.

XX

PR 12-JUN-1991; 91US-00713716.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Maloy WL, Kari UP;

XX

DR WPI; 1993-017904/02.

XX

PT New C-terminal-substd. amphiphilic peptide(s) - for treating bacterial,
PT viral or fungal infections and tumours, also useful as spermicide.

XX

PS Claim 21; Page 114; 124pp; English.

XX

CC This peptide is a preferred example of a highly generic amphiphilic
CC peptide with a C-terminal modification which increases the peptide's
CC biological activity c.f. the unmodified peptide. The preferred C-terminal
CC modification is -(CO)-NHCH2CH2OH or -(CO)-NHCH2CH2NH2. Such substd.
CC peptides may be used for inhibiting the growth of a target cell, virus or
CC virally-infected cell in a host. The peptides have a broad range of
CC potent antibiotic activity, e.g. against gram- negative and gram-positive
CC bacteria, fungi, protozoa and parasites. The peptides can also be used to
CC promote wound healing and treatment of burns. Other preferred amphiphilic
CC peptides include magainins and their analogues, PGLa, XPF, CPF, a
CC cecropin and a sarcotoxin. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 1 AKK 3

RESULT 23

AAR34255

ID AAR34255 standard; peptide; 11 AA.

XX

AC AAR34255;

XX

DT 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX

DE Mutant HTLV-I residues 88-98, peptide 2L-1.9.

XX

KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.

XX

OS Synthetic.

XX

PN WO9306843-A1.

XX

PD 15-APR-1993.

XX

PF 08-OCT-1992; 92WO-US008405.

XX

PR 08-OCT-1991; 91US-00771553.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Parker TJ, Haynes BF;

XX
DR WPI; 1993-134125/16.
XX
PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.
XX
PS Example 7; Page 32; 50pp; English.
XX
CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RNA 11
|||
Db 7 RNA 9

RESULT 24
AAR34248
ID AAR34248 standard; peptide; 11 AA.
XX
AC AAR34248;
XX
DT 25-MAR-2003 (revised)
DT 04-AUG-1993 (first entry)
XX
DE Mutant HTLV-I residues 88-98, peptide 2L-1.2.
XX
KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.
XX
OS Synthetic.
XX
PN WO9306843-A1.
XX
PD 15-APR-1993.
XX
PF 08-OCT-1992; 92WO-US008405.
XX
PR 08-OCT-1991; 91US-00771553.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Palker TJ, Haynes BF;
XX
DR WPI; 1993-134125/16.

XX
PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX
PS Example 7; Page 32; 50pp; English.

XX
CC To determine which amino acids within the HTLV-I envelope amino acids 88-
CC 98 were required for absorption of neutralising anti-peptide antibodies
CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which
CC sequential amino acids were each replaced by the amino acid alanine.
CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native
CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93
CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
Db 2 AKK 4

RESULT 25

AAR41495

ID AAR41495 standard; peptide; 11 AA.

XX
AC AAR41495;

XX
DT 23-FEB-1994 (first entry)

XX
DE TNF inhibitory peptide VII.

XX
KW Tumour necrosis factor; TNF; inhibition; solid phase synthesis; ss.

XX
OS Synthetic.

XX
PN JP05194594-A.

XX
PD 03-AUG-1993.

XX
PF 21-JAN-1992; 92JP-00029044.

XX
PR 21-JAN-1992; 92JP-00029044.

XX
PA (SAGA) SAGAMI CHEM RES CENTRE.

XX
DR WPI; 1993-282916/36.

XX
PT TNF inhibitory novel peptide(s) - include N-terminal amino Gp. which is
PT opt. modified with acetyl, T-butoxy-carbonyl or benzyl-oxy-carbonyl Gp.
PT and C-terminal carboxy Gp. is opt. amidated.

XX
PS Claim 1; Page 6; 8pp; Japanese.

XX
CC The sequences given in AAR41489-99 are tumour necrosis factor (TNF)
CC inhibitory peptides. They may optionally be modified at the N- terminal
CC with an acetyl, t-butoxycarbonyl or benzyloxycarbonyl, and at the C-
CC terminal they are optionally amidated. These peptides are produced by
CC solid phase synthesis methods and may be produced at low cost
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
|||
Db 3 AKK 5

RESULT 26
AAR31493
ID AAR31493 standard; protein; 11 AA.
XX
AC AAR31493;
XX
DT 25-MAR-2003 (revised)
DT 26-MAY-1993 (first entry)
XX
DE P3 OF 31-34 bovine subunit D N-terminal fragment #7.
XX
KW Subunit; D; A; C; B; P3 OF 31-34; osteogenic; active; protein; bone;
KW heterodimer; disulphide bond; formation; repair; defect; human; bovine;
KW primer; probe.
XX
OS Synthetic.
XX
PN WO9300049-A1.
XX
PD 07-JAN-1993.
XX
PF 01-JUL-1991; 91WO-US004686.
XX
PR 20-JUN-1991; 91US-00718274.
XX
PA (XOMA) XOMA CORP.
XX
PI Grinna L, Theofan G, Parsons TF;
XX
DR WPI; 1993-036101/04.
XX
PT Osteogenically active protein preparations for repairing bone defects -
PT comprise hetero-dimer of P3 OF 31-34 sub-unit B and P3 OF 31-34 sub-unit
PT D.
XX
PS Disclosure; Page 34; 107pp; English.
XX
CC The sequences given in AAR31493-95 represent the first 11 amino acids
CC from the amino terminus and two internal fragments of bovine subunit D of

CC P3 OF 31-34. These sequences were used to design primers and a probe (see
CC also AAQ39242 and AAQ34517-18) which were used in the isolation of the
CC bovine subunit D cDNA sequence. P3 OF 31-34 is an osteogenically active
CC protein. A primary osteogenically active peptide is formed of a
CC heterodimer of P3 OF 31-34 subunits B and D which are linked by at least
CC one disulphide bond. The B/D heterodimer stimulates osteogenesis and can
CC be used to induce bone formation in mammals, to repair bone defects.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
|||
Db 5 KQR 7

RESULT 27

AAR35026

ID AAR35026 standard; peptide; 11 AA.

XX

AC AAR35026;

XX

DT 02-AUG-1993 (first entry)

XX

DE GMP-140 MAb FR6.

XX

KW Complementarity determining region; CDR; human; GMP-140; antigen; MAb;
KW monoclonal antibody; framework region; FR.

XX

OS Synthetic.

XX

PN JP05070498-A.

XX

PD 23-MAR-1993.

XX

PF 03-APR-1991; 91JP-00096176.

XX

PR 03-APR-1991; 91JP-00096176.

XX

PA (TAKI) TAKARA SHUZO CO LTD.

XX

DR WPI; 1993-131304/16.

XX

PT New polypeptide - specifying MAb antigen-recognising site of human GMP-
PT 140.

XX

PS Disclosure; Page 7; 10pp; Japanese.

XX

CC The sequences given in AAR35023-30 represent the framework regions (FRs)
CC from a novel polypeptide which recognises human GMP-140. The poly-
CC peptides are monoclonal antibodies (MAb) (see also AAQ39233-34) and are
CC used to recognise specific GMP-140 antigens

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
|||
Db 1 KQR 3

RESULT 28

AAR45132

ID AAR45132 standard; peptide; 11 AA.

XX

AC AAR45132;

XX

DT 25-MAR-2003 (revised)

DT 28-JUN-1994 (first entry)

XX

DE Amphiphilic peptide for N-terminal lipophilic substitution.

XX

KW Ion channel; magainin; PGLa; XPF; CPF; cecropin; sarcotoxin; amphiphilic;
KW hydrophobic; hydrophilic; lipophilic; growth; inhibition; target cell;
KW virus; virally-infected cell; antimicrobial; antiviral; antitumour;
KW antiparasitic; spermicide; wound healing; burn; infection.

XX

OS Synthetic.

XX

PN WO9324138-A1.

XX

PD 09-DEC-1993.

XX

PF 27-MAY-1993; 93WO-US005192.

XX

PR 01-JUN-1992; 92US-00891201.

XX

PA (MAGA-) MAGAININ PHARM INC.

XX

PI Kari U;

XX

DR WPI; 1993-405419/50.

XX

PT Peptide(s) or proteins with an N-terminal lipophilic substit. - used for
PT inhibiting growth of target cell, virus or virally-infected cell.

XX

PS Disclosure; Page 97-103; 113pp; English.

XX

CC A novel compsn. for inhibiting growth of a target cell, virus or virally-
CC infected cell comprises a peptide of formula T-N(W)-X (I). X is a
CC biologically active amphiphilic ion channel-forming peptide or protein;
CC pref. a magainin peptide, a PGLa peptide, a XPF peptide, a CPF peptide, a
CC cecropin or a sarcotoxin. N is the nitrogen of the N-terminal amino
CC group. T is a lipophilic moiety; pref. R-CO, where R is a 2-16C
CC hydrocarbon (alkyl or aromatic or alkylaromatic). T is pref. an octanoyl
CC group. W is T or hydrogen. Amphiphilic peptides as examples of X are
CC given in AAR45115-138. The N-terminal subst. peptides and proteins have

CC increased biological activity as compared with unsubstd. peptides or
CC proteins or peptides substd. at the N-terminal with an acetyl gp. They
CC can be used as antimicrobial agents, antiviral agents, antitumour agents,
CC antiparasitic agents or spermicides and can also exhibit other bioactive
CC functions. They can also be used in promoting or stimulating wound
CC healing, for the treatment of external burns and to treat and/or prevent
CC skin and burn infections or eye infections. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 1 AKK 3

RESULT 29

AAR60841

ID AAR60841 standard; peptide; 11 AA.

XX

AC AAR60841;

XX

DT 25-MAR-2003 (revised)

DT 05-JUN-1995 (first entry)

XX

DE Polyoxime octa-GXL baseplate.

XX

KW Polyoxime; homopolyoxime; heteropolyoxime; peptide presentation;
KW cell imaging; complementary orthogonal specifically active molecule;
KW COSM; baseplate; immunogen.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
FT	Modified-site	1
FT		/label= OTHER
FT		/note= "glyoxyl-glycine"
FT	Modified-site	4
FT		/label= OTHER
FT		/note= "glyoxyl-lysine"
FT	Modified-site	5
FT		/label= OTHER
FT		/note= "glyoxyl-lysine"
FT	Modified-site	6
FT		/label= OTHER
FT		/note= "glyoxyl-lysine"
FT	Modified-site	7
FT		/label= OTHER
FT		/note= "glyoxyl-lysine"
FT	Modified-site	8
FT		/label= OTHER
FT		/note= "glyoxyl-lysine"
FT	Modified-site	9

FT /label= OTHER
FT /note= "glyoxyl-lysine"
FT Modified-site 10
FT /label= OTHER
FT /note= "glyoxyl-lysine"
XX
PN WO9425071-A1.
XX
PD 10-NOV-1994.
XX
PF 05-MAY-1994; 94WO-IB000093.
XX
PR 05-MAY-1993; 93US-00057594.
PR 31-AUG-1993; 93US-00105904.
PR 31-AUG-1993; 93US-00114877.
XX
PA (ROSE/) ROSE K.
PA (OFFO/) OFFORD R E.
XX
PI Rose K, Offord RE;
XX
DR WPI; 1994-357918/44.
XX
PT Homo- and hetero-polyoxime compounds and their preparation - used for
PT peptide presentation to antibodies and in cell imaging etc.
XX
PS Disclosure; Page 53; 85pp; English.
XX
CC Peptides given in AAR60833-62 are used as baseplates and COSMs for the
CC preparation of polyoximes having varying spacing, charge, lipophilicity,
CC valency, conformational restraints, solubility and other physical and
CC biological properties. An octa-GXL baseplate structure is given in
CC AAR60841. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps. 0;

Qy 2 KKK 4
|||
Db 4 KKK 6

RESULT 30
AAR50563
ID AAR50563 standard; peptide; 11 AA.
XX
AC AAR50563;
XX
DT 25-MAR-2003 (revised)
DT 18-OCT-1994 (first entry)
XX
DE Amphiphilic peptide #112.
XX
KW Amphiphilic; ion forming; gynaecological malignancy; magainin; PGLa; XPF;

KW CPF; cecropin; sarcotoxin; melittin; apidaecin; defensin;
KW major basic protein; eosinophils; uterine; cervical; cancer;
KW bacterial permeability increasing protein; ovarian; stage IC.
XX
OS Synthetic.
XX
PN WO9405313-A1.
XX
PD 17-MAR-1994.
XX
PF 16-AUG-1993; 93WO-US007798.
XX
PR 31-AUG-1992; 92US-00937462.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Jacob LS, Maloy WL, Baker MA;
XX
DR WPI; 1994-100851/12.
XX
PT Treating gynaecological tumours with amphiphilic peptide(s) - which form
PT ion channels, e.g. magainin or PGLa peptide(s), partic. for treating
PT ovarian, uterine or cervical cancers.
XX
PS Disclosure; Page 116; 130pp; English.
XX
CC The sequences given in AAR50452-568 represent amphiphilic, ion forming
CC peptides which may be used to treat gynaecological malignancy. These
CC peptides are based on magainin, PGLa, XPF or CPF, a cecropin, a
CC sarcotoxin, melittin, an apidaecin, a defensin, major basic protein of
CC eosinophils or a bacterial permeability increasing protein. These
CC peptides are esp. used to treat ovarian, esp. stage IC, uterine or
CC cervical cancers. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 31
AAR55987
ID AAR55987 standard; peptide; 11 AA.
XX
AC AAR55987;
XX
DT 25-MAR-2003 (revised)
DT 19-DEC-1994 (first entry)
XX
DE Ion channel forming peptide.
XX
KW Ion channel forming peptide; tumour; skin disease; malignancy; melanoma;

KW carcinoma; basal cell; squamous cell; magainin; PGLa; CPF peptides;
KW cercopins; sarcotoxin; mellitin; apidocin; defensins;
KW major basic protein; bacteria-permeability increasing protein; perforin.

XX
OS Synthetic.

XX
PN WO9412206-A1.

XX
PD 09-JUN-1994.

XX
PF 03-DEC-1993; 93WO-US011885.

XX
PR 03-DEC-1992; 92US-00984957.

XX
PA (MAGA-) MAGAININ PHARM INC.

XX
PI Jacob LS, Maloy WL;

XX
DR WPI; 1994-199965/24.

XX
PT Treating skin cancer with ion channel forming peptide(s) - e.g.
PT magainins, mellitin etc., specifically for treating melanoma.

XX
PS Disclosure; Page 121; 136pp; English.

XX
CC The peptide is used to treat dermatological malignancies. It may be used
CC to treat especially melanoma but also basal cell and squamous cell
CC carcinomas. It can be used together with an ion which also
CC inhibits/prevents growth of the target cell. Peptides used for such
CC therapy include magainin, PGLa or CPF peptides; cercopins, sarcotoxins,
CC mellitin, apidocins, defensins, major basic protein of eosinophils;
CC bacteria-permeability increasing protein and perforin. See also AAQ55876-
CC Q55997. (Updated on 25-MAR-2003 to correct PN field.)

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 32

AAR59065

ID AAR59065 standard; peptide; 11 AA.

XX
AC AAR59065;

XX
DT 25-MAR-2003 (revised)
DT 21-APR-1995 (first entry)

XX
DE Cancer treating, amphiphilic ion-channel forming peptide.

XX
KW Amphiphilic ion-channel forming peptide; cancer treatment;

KW protease inhibitors.
XX
OS Synthetic.
XX
PN WO9419369-A1.
XX
PD 01-SEP-1994.
XX
PF 22-FEB-1994; 94WO-US002121.
XX
PR 26-FEB-1993; 93US-00021607.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Herlyn M, Jacob LS, Maloy WL;
XX
DR WPI; 1994-294258/36.
XX
PT Treating cancerous growths - by administering biologically active
PT peptide(s) and protease inhibitors.
XX
PS Claim 2; Page 106; 124pp; English.
XX
CC AAR59060 to AAR59066 are a group of amphiphilic ion-channel forming
CC peptides conforming to the same generic sequence. Used in combination
CC with one or more protease inhibitors and other amphiphilic ion-channel
CC forming peptides or proteins; they are effective in the treatment of
CC cancerous growths. In particular during surgery and radiation treatment
CC they may be useful in inhibiting, preventing and/or destroying potential
CC "loose" malignant cells capable of colonising other sites. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 33
AAR56948
ID AAR56948 standard; peptide; 11 AA.
XX
AC AAR56948;
XX
DT 25-MAR-2003 (revised)
DT 17-MAR-1995 (first entry)
XX
DE Peptide which neutralises bacterial endotoxin.
XX
KW septic shock; bacterial endotoxin; lipopolysaccharide; LPS;
KW gram negative bacteria; conjugate moiety; septicemia; neutralising;
KW longer activity; polyvinylpyrrolidone; dextran; hetastarch;

KW polyvinyl alcohol; ion-channel forming; amphiphilic.
XX
OS Synthetic.
XX
PN WO9413697-A1.
XX
PD 23-JUN-1994.
XX
PF 06-DEC-1993; 93WO-US011841.
XX
PR 07-DEC-1992; 92US-00987443.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Hendi M, Rao M, Williams TJ;
XX
DR WPI; 1994-217804/26.
XX
PT New conjugates of bioactive amphiphilic peptide(s) and conjugate moiety -
PT are useful for treatment of septic shock.
XX
PS Disclosure; Page 115; 141pp; English.
XX
CC Septic shock is often due to the body's reaction to foreign
CC lipopolysaccharide (LPS). The compounds of the invention neutralise
CC bacterial endotoxins without neutralising essential proteins in the
CC plasma of patients, eg. heparins. They also have longer duration of
CC activity than unconjugated peptides. In general peptides such as this are
CC ion-channel forming peptides. The compounds are biologically active
CC peptides linked to a conjugate moiety, eg. carbohydrates, proteins,
CC polyvinylpyrrolidone, polyalkylene glycols and polyvinyl alcohols. The
CC conjugate moiety may be linked at the C- or N-terminal or internally of
CC the peptide. AAR55591-631 and AAR56879-957 are examples of these peptide-
CC conjugate moiety compounds (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 34
AAR59984
ID AAR59984 standard; peptide; 11 AA.
XX
AC AAR59984;
XX
DT 25-MAR-2003 (revised)
DT 26-MAR-1995 (first entry)
XX
DE Myc-tag peptide tag.
XX

KW Marker; antibody; single chain Fv fusion protein; sFv.
XX
OS Synthetic.
XX
PN WO9415642-A1.
XX
PD 21-JUL-1994.
XX
PF 07-JAN-1994; 94WO-US000261.
XX
PR 08-JAN-1993; 93US-00002324.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI George AJT, Segal DM, Huston JS;
XX
DR WPI; 1994-248905/30.
XX
PT Delivering agents to target cells - where monospecific binding proteins
PT are administered to a host and bind to target cells, followed by admin.
PT of multivalent antibodies to direct the agents to the target cells.
XX
PS Disclosure; Page 46; 80pp; English.
XX
CC The sequence is that of the myc-tag peptide sequence which is used as a
CC peptide tag to serve as a contact for association with a recognition site
CC on a multivalent antibody, thus directing the multivalent antibody to
CC bind to a target cell. See also AAR59985-6. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 35
AAR50448
ID AAR50448 standard; peptide; 11 AA.
XX
AC AAR50448;
XX
DT 25-MAR-2003 (revised)
DT 17-OCT-1994 (first entry)
XX
DE Amphiphilic peptide #113.
XX
KW Amphiphilic peptide; aprotic organic solvent; alcohol; antitumour;
KW antibiotic; antimicrobial; antifungal; antiparasitic; anticancer;
KW antiviral; human; animal; plant; ion-channel; forming peptide.
XX

OS Synthetic.
XX
PN WO9405308-A1.
XX
PD 17-MAR-1994.
XX
PF 13-AUG-1993; 93WO-US007694.
XX
PR 28-AUG-1992; 92US-00936504.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Williams JI;
XX
DR WPI; 1994-100846/12.
XX
PT Purifying amphiphilic protein or peptide by solvent extrn. - partic. for
PT recombinant, ion-channel forming peptide(s) such as magainins, avoids use
PT of chaotropic agents.
XX
PS Disclosure; Page 124; 135pp; English.
XX
CC The sequences given in AAR50336-451 are amphiphilic peptides which were
CC isolated by the method of the invention. A material containing
CC amphiphilic peptides such as these, was treated with a mixt. of aprotic
CC organic solvent and alcohol to form a single miscible solution. This
CC solution was then treated with a aqueous solution to form an aqueous
CC phase solution containing the peptides and an organic solvent phase, and
CC the peptides were isolated from the aqueous phase. The isolated peptides
CC may be useful as antibiotic, antimicrobial, antifungal, antiparasitic,
CC antitumour, anticancer, and/or antiviral agents for treatment of humans,
CC animals or plants. These peptides are esp. ion-channel forming peptides
CC which enable biologically active ions to enter cells. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 36
AAR72301
ID AAR72301 standard; peptide; 11 AA.
XX
AC AAR72301;
XX
DT 25-MAR-2003 (revised)
DT 20-OCT-1995 (first entry)
XX
DE Anti-HIV MBPC.3.
XX

KW Multiple branch peptide construction; MBPC; HIV-1;
KW human immunodeficiency virus type 1; virucide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .6
FT /note= "peptide is present 168 times, each attached to 1
FT of 8 lysine residues (position 7), in dendritic
FT structure"
FT Misc-difference 7
FT /note= "lysine at position 7 is present 8 times, each
FT attached to 1 of 4 other lysine residues (position 8) and
FT also to 1 of 16 peptide moieties (position 1-6) in
FT dendritic structure"
FT Misc-difference 8
FT /note= "lysine at position 8 is present 4 times, each
FT attached to other lysines (positions 7 and 9) in
FT dendritic structure"
FT Misc-difference 9
FT /note= "lysine at position 9 is present 2 times, each
FT attached to 1 of 4 other lysine residues (position 8) and
FT to a core lysine residue (position 10), in dendritic
FT structure"
FT Modified-site 11
FT /label= bAla, bAla-NH2
XX
PN WO9507929-A1.
XX
PD 23-MAR-1995.
XX
PF 13-SEP-1994; 94WO-GB001992.
XX
PR 13-SEP-1993; 93GB-00018901.
PR 15-JUN-1994; 94US-00260086.
XX
PA (ARME-) ARMEL SA.
PA (MCKE/) MCKELVEY I E.
XX
PI Sabatier JM, Benjouad A, Yahi N, Fenouillet E, Mabrouk K;
PI Gluckman J, Van Rietschoten J, Rochat H;
XX
DR WPI; 1995-131312/17.
XX
PT Multiple branch peptide constructions formed from the V3 loop of HIV-1
PT gp120 - used to treat HIV infection.
XX
PS Disclosure; Page 5; 39pp; English.
XX
CC Multiple branch peptide constructions (given in AAR72299-301) are formed
CC from the V3 loop of HIV-1 gp120. Each MBPC includes multiple peptide
CC moieties incorporating the GPGR consensus sequence, each attached to the
CC amino group of a lysine residue, forming a dendritic structure. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 7 KKK 9

RESULT 37

AAR72299

ID AAR72299 standard; peptide; 11 AA.

XX

AC AAR72299;

XX

DT 25-MAR-2003 (revised)

DT 20-OCT-1995 (first entry)

XX

DE Anti-HIV MBPC.1.

XX

KW Multiple branch peptide construction; MBPC; HIV-1;

KW human immunodeficiency virus type 1; virucide.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 1. .7

FT /note= "peptide is present 8 times, each attached to 1 of 4 lysine residues (position 8), in dendritic structure"

FT Misc-difference 8

FT /note= "lysine at position 8 is present 4 times, each attached to 1 of 2 other lysine residues (position 9) and also to 1 of 8 peptide moieties (positions 1-7), in dendritic structure"

FT Misc-difference 9

FT /note= "lysine at position 9 is present 2 times, each attached to 1 of 4 other lysine residues (position 8) and to a core lysine residue (position 10), in dendritic structure"

FT Modified-site 11

FT /label= bAla, bAla-NH2

XX

PN WO9507929-A1.

XX

PD 23-MAR-1995.

XX

PF 13-SEP-1994; 94WO-GB001992.

XX

PR 13-SEP-1993; 93GB-00018901.

PR 15-JUN-1994; 94US-00260086.

XX

PA (ARME-) ARMEL SA.

PA (MCKE/) MCKELVEY I E.

XX

PI Sabatier JM, Benjouad A, Yahi N, Fenouillet E, Mabrouk K;

PI Gluckman J, Van Rietschoten J, Rochat H;

XX

DR WPI; 1995-131312/17.

XX

PT Multiple branch peptide constructions formed from the V3 loop of HIV-1
PT gp120 - used to treat HIV infection.

XX

PS Disclosure; Page 5; 39pp; English.

XX

CC Multiple branch peptide constructions (given in AAR72299-301) are formed
CC from the V3 loop of HIV-1 gp120. Each MBPC includes multiple peptide
CC moieties incorporating the GPGR consensus sequence, each attached to the
CC amino group of a lysine residue, forming a dendritic structure. (Updated
CC on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||

Db 8 KKK 10

RESULT 38

AAR68911

ID AAR68911 standard; peptide; 11 AA.

XX

AC AAR68911;

XX

DT 25-MAR-2003 (revised)

DT 06-AUG-1995 (first entry)

XX

DE Factor-VII-derived peptide fragment FVII-1.

XX

KW Factor-VII; blood-clotting factor; thrombosis; angina;
KW cerebrovascular disease; pulmonary embolism; heart disease.

XX

OS Synthetic.

XX

PN WO9500541-A1.

XX

PD 05-JAN-1995.

XX

PF 17-JUN-1994; 94WO-GB001315.

XX

PR 18-JUN-1993; 93GB-00012601.

PR 10-MAY-1994; 94GB-00009335.

XX

PA (HAFS-) HAFSLUND NYCOMED AS.

PA (HOLM/) HOLMES M J.

XX

PI Stephens RW, Orning L, Sakariassen KS;

XX

DR WPI; 1995-052003/07.

XX

PT Factor VII-derived peptide compounds - useful for preventing/inhibiting

PT binding of tissue factor to factor VII.
XX
PS Disclosure; Page 20; 61pp; English.
XX
CC This peptide fragment is useful for preparing pharmaceutical compositions
CC for prevention or inhibition of Factor-VII binding to tissue factor. It
CC is useful for treating or preventing blood clotting disorders in humans
CC and animals, e.g. thrombosis, angina, cerebrovascular disease or
CC pulmonary embolism. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RNA 11
|||
Db 9 RNA 11

RESULT 39
AAR66766
ID AAR66766 standard; peptide; 11 AA.
XX
AC AAR66766;
XX
DT 25-MAR-2003 (revised)
DT 06-SEP-1995 (first entry)
XX
DE Zinc-finger peptide Y-13-K from murine Kin17 protein.
XX
KW chromosomal rearrangement; kin17 protein; SOS DNA repair system; RecA;
KW genotoxic agent; zinc finger; DNA binding protein.
XX
OS Mus musculus.
XX
PN FR2706487-A1.
XX
PD 23-DEC-1994.
XX
PF 15-JUN-1993; 93FR-00007171.
XX
PR 15-JUN-1993; 93FR-00007171.
XX
PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI Angulo-Mora JF, Tissier A, Frelat G, Mauffrey P, Guilly M;
XX
DR WPI; 1995-039031/06.
XX
PT Purified murine kin17 protein prepn. for detecting chromosomal
PT rearrangements - also related antibodies, human and murine DNA, primers,
PT probes and vectors, used to assess damage caused by genotoxic agents.
XX
PS Claim 4; Page 31; 54pp; French.
XX

CC The murine Kin17 protein includes a zinc finger domain (see AAR66766),
CC recognises single- and double-stranded DNA (partic. regions of secondary
CC structure), has apparent mol. wt. 43 kD and is recognised by both anti-
CC kin17 antibodies and antibodies against the RecA protein of E.coli. The
CC Kin17 protein is involved in DNA repair; it can be used to monitor
CC chromosomal rearrangements following exposure to genotoxic agents.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QKQ 8
|||
Db 1 QKQ 3

RESULT 40

AAR84083

ID AAR84083 standard; peptide; 11 AA.

XX

AC AAR84083;

XX

DT 12-JUN-1996 (first entry)

XX

DE Human lactoferrisin antibacterial peptide.

XX

KW Recombinant vector; human; lactoferrisin; antibacterial peptide;
KW regulatory sequence; tac; promoter; shuttle; vector; pGEX2; GALL; pKOM2;
KW Rous Sarcoma Virus; long terminal repeat; pRSVNot; lactoferricin.

XX

OS Homo sapiens.

XX

PN JP07274970-A.

XX

PD 24-OCT-1995.

XX

PF 01-APR-1994; 94JP-00085244.

XX

PR 01-APR-1994; 94JP-00085244.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

DR WPI; 1995-399338/51.

XX

PT Recombinant vector contg. lactoferrisin gene - used to prepare an
PT antibacterial peptide.

XX

PS Disclosure; Page 11; 18pp; Japanese.

XX

CC A recombinant vector in which a DNA sequence encoding at least the
CC generic lactoferrisin antibacterial peptide AAR88216 (specific examples
CC of which are given in AAR84083-85) is inserted, pref. downstream of the
CC vector's regulatory sequence, is claimed. Pref. examples of amino acid
CC sequences contg. the above peptide are given in AAR88217/18. The

CC regulatory sequence is the tac promoter from shuttle vector pGEX2, the
CC GAL1 promoter from vector pKOM2 or Rous Sarcoma Virus long terminal
CC repeat from vector pRSVNot
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QRN 10
Db 6 QRN 8

RESULT 41
AAR67858
ID AAR67858 standard; peptide; 11 AA.
XX
AC AAR67858;
XX
DT 25-MAR-2003 (revised)
DT 07-SEP-1995 (first entry)
XX
DE FVII/TF multi-protein complex inhibition test peptide FVII-1.
XX
KW Factor VII; Factor 7; blood clotting factor; multi-protein complex;
KW human tissue factor; FVII/TF; assay.
XX
OS Synthetic.
XX
PN WO9500847-A1.
XX
PD 05-JAN-1995.
XX
PF 17-JUN-1994; 94WO-GB001314.
XX
PR 18-JUN-1993; 93GB-00012638.
XX
PA (HAFS-) HAFSLUND NYCOMED AS.
PA (HOLM/) HOLMES M J.
XX
PI Stephens R, Oerning L, Sakariassen K;
XX
DR WPI; 1995-052226/07.
XX
PT Immunoassay for multi-protein complexes - used to detect malfunction in
PT formation of complexes in an individual, e.g. due to genetic or
PT physiological disorders..
XX
PS Example 2; Page 8; 19pp; English.
XX
CC Synthetic peptides (AAR67858-R67865) were individually assayed as test
CC substances to ascertain their effect on the formation of the blood-
CC clotting factor VII/tissue factor multi-protein complex. Of the peptides
CC tested, the most inhibition was obtained with cyclic peptides
CC representing the ring structures present in the FVII growth factor

CC domains (i.e. AAR67861, AAR67864 and AAR67863). Peptide AAR67858, a
CC linear peptide corresp. to residues 136-146 from a region close to the
CC site of cleavage which activates FVII also had good inhibitory activity.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RNA 11
|||
Db 9 RNA 11

RESULT 42

AAW21466

ID AAW21466 standard; peptide; 11 AA.

XX

AC AAW21466;

XX

DT 29-JUL-1997 (first entry)

XX

DE Islet amyloid precursor derived signal oligopeptide #4.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Homo sapiens.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI RATH M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).

XX
PS Claim 5; Page 67; 88pp; English.

XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligopeptides. These signal oligopeptides are localised on the surface of the protein and are represented by the hydrophilicity maxima of the protein. These peptides are enriched in charged amino acids arranged with neutral spacer amino acids. The specific signal character of these oligopeptides is determined by a characteristic combination of conformation and charge within the signal sequence. These oligopeptides may be used as vaccines in the treatment of human disease, as competitive inhibitors to prevent or reduce the metabolic action or interaction of a selected protein by blocking its specific signal sequences, or as therapeutic agents to function as feedback regulators to reduce synthesis rate of a selected protein. These peptides may be modified by omitting one or more amino acids at the N- and/or C-terminal, by substituting one or more amino acids without consideration of charge and polarity, by substituting one or more amino acids with amino acid residues with similar charge and/or polarity, by omitting one or more amino acids or a combination of these

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RNA 11
|||
Db 2 RNA 4

RESULT 43

AAW21220
ID AAW21220 standard; peptide; 11 AA.

XX
AC AAW21220;

XX
DT 29-JUL-1997 (first entry)

XX
DE Farnesyl synthetase derived signal oligopeptide #20.

XX
KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV; competitive inhibitor; feedback regulator; synthesis; gastrin precursor; charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1; hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus; gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin; Alzheimer amyloid A4; corticotropin releasing factor binding protein; apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS; herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A; Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide; fibroblast MMP1; schistosoma elastase precursor; schistosomin; hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX
OS Homo sapiens.

XX
PN WO9519568-A1.

PD 20-JUL-1995.
XX
PF 12-JAN-1995; 95WO-US000575.
XX
PR 14-JAN-1994; 94US-00182248.
XX
PA (RATH/) RATH M.
XX
PI Rath M;
XX
DR WPI; 1995-263953/34.
XX
PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).
XX
PS Claim 5; Page 26; 88pp; English.
XX
CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
Db 9 AKK 11

RESULT 44
AAW21471
ID AAW21471 standard; peptide; 11 AA.
XX
AC AAW21471;
XX
DT 30-JUL-1997 (first entry)
XX
DE Collagenase (fibroblast MMP1) derived signal oligopeptide #3.
XX
KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;

KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor; KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1; KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus; KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin; KW Alzheimer amyloid A4; corticotropin releasing factor binding protein; KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS; KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A; KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide; KW fibroblast MMP1; schistosoma elastase precursor; schistosomin; KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Homo sapiens.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as PT regions of max. hydrophilicity, used in modulating communication between PT protein(s).

XX

PS Claim 5; Page 68; 88pp; English.

XX

CC The sequences given in AAW21201-560 represent hydrophilic signal oligo- CC peptides. These signal oligopeptides are localised on the surface of the CC protein and are represented by the hydrophilicity maxima of the protein. CC These peptides are enriched in charged amino acids arranged with neutral CC spacer amino acids. The specific signal character of these oligopeptides CC is determined by a characteristic combination of conformation and charge CC within the signal sequence. These oligopeptides may be used as vaccines CC in the treatment of human disease, as competitive inhibitors to prevent CC or reduce the metabolic action or interaction of a selected protein by CC blocking its specific signal sequences, or as therapeutic agents to CC function as feedback regulators to reduce synthesis rate of a selected CC protein. These peptides may be modified by omitting one or more amino CC acids at the N- and/or C-terminal, by substituting one or more amino CC acids without consideration of charge and polarity, by substituting one CC or more amino acids with amino acid residues with similar charge and/or CC polarity, by omitting one or more amino acids or a combination of these

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

7 KQR 9

RESULT 45

AAR76917

ID AAR76917 standard; peptide; 11 AA.

XX

AC AAR76917;

XX

DT 08-MAR-1996 (first entry)

XX

DE Thymosin alpha-1 peptide analogue #23.

XX

KW Thymosin alpha-1; analogue; immune system modulator; alpha-interferon; gamma-interferon; macrophage migration inhibitory factor; T-cell marker; interleukin-2 receptor; helper T-cell; solid phase synthesis; immunodeficiency; therapy; AIDS; HIV; immunodepravation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "optionally amidated Pro or amidated Gly"

XX

PN WO9520602-A2.

XX

PD 03-AUG-1995.

XX

PF 18-JAN-1995; 95WO-US000617.

XX

PR 28-JAN-1994; 94US-00188232.

XX

PA (ALPH-) ALPHA 1 BIOMEDICALS INC.

XX

PI Wang S;

XX

DR WPI; 1995-275412/36.

XX

PT New thymosin alpha-1 peptide analogues - for the treatment of immunodeficiency diseases and the reconstitution of immune functions in immuno-depressed patients.

XX

PS Claim 7; Page ?; 24pp; English.

XX

CC The sequences represented by AAR76895-R76935 are thymosin alpha-1 analogues. Thymosin alpha-1 is an immune system modulator. Thymosin alpha-1 activity includes, stimulation of alpha- and gamma-interferon production, increasing macrophage migration inhibitory factor production, inducing expression of T-cell markers (including interleukin-2 receptors), and improving helper T-cell activity. These sequences function like natural thymosin alpha-1, and are easy to produce. These sequences were synthesised by solid phase synthesis on a 4-methylbenzhydrylamine resin. The peptides were cleaved from this resin using trifluoromethane sulfonic acid (TFS). These sequences can be used to reconstitute immune functions in immunodeprived and immunodepressed patients. They can also be used in the treatment of immunodeficiency

CC diseases
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
|||
Db 1 KKE 3

RESULT 46

AAR79718

ID AAR79718 standard; peptide; 11 AA.

XX
AC AAR79718;

XX
DT 27-FEB-1996 (first entry)

XX
DE Optimal peptide substrate for cyclin containing kinases.

XX
KW Peptide library; phosphorylation site; protein kinase; substrate;
KW inhibitor; competitor; cellular response; cell cycle control;
KW immune response; transcriptional activation; cell development.

XX
OS Synthetic.

XX
PN WO9518823-A2.

XX
PD 13-JUL-1995.

XX
PF 06-JAN-1995; 95WO-US000147.

XX
PR 07-JAN-1994; 94US-00178570.

XX
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX
PI Cantley LC, Songyang Z;

XX
DR WPI; 1995-255036/33.

XX
PT Determn.of amino acid sequence of protein kinase phosphorylation site -
PT by phosphorylation of peptide library and sequencing phospho:peptide(s)
PT formed, also new substrates and their analogues for modulating or
PT detecting protein kinase.

XX
PS Example 10; Page 40; 131pp; English.

CC An oriented degenerate peptide library of the amino acid formula AAR79661
CC was constructed to isolate the amino acid sequences at the
CC phosphorylation sites of a protein kinase eg. protein kinase A, cyclin
CC B/p33(cdc2), src family kinases, etc. Peptides which are phosphorylated
CC are isolated and their amino acid sequences are compared to known
CC substrate/inhibitor peptide sequences for that protein kinase. The
CC peptides AAR79718-R79721 are synthetic peptides designed to be optimal

CC substrates for a range of protein kinases. This peptide sequence is
CC designed as a substrate for cyclin containing kinases, e.g cyclin
CC B/p33(cdc2) or cyclin A/p33(CDK2). The isolated peptides can be used to
CC screen cpds. for effects on the protein kinase activity, generate
CC antibodies to identify native kinase substrates, or modulate a variety of
CC cellular responses in which protein kinases are involved eg. cell cycle
CC control, immune response, transcriptional activation or cell development
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 8 KKK 10

RESULT 47

AAR90267

ID AAR90267 standard; peptide; 11 AA.

XX

AC AAR90267;

XX

DT 10-JUL-1996 (first entry)

XX

DE Ion-channel forming peptide #128 with lipophilic N-terminal group.

XX

KW Ion channel forming peptide; lipophilic; N-terminal modification;
KW magainin; inhibition; cell growth; viral replication; ionophore;
KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;
KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal amino group is mono- or di-substd. by
FT lipophilic moiety, esp. octanoyl"

XX

PN WO9519370-A1.

XX

PD 20-JUL-1995.

XX

PF 18-JAN-1995; 95WO-US000714.

XX

PR 18-JAN-1994; 94US-00184462.

XX

PA (MAGA-) MAGAININ PHARM INC..

XX

PI Kari U, Williams TJ, McLane M;

XX

DR WPI; 1995-263826/34.

XX

PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic
PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or

PT antitumour agents.

XX

PS Claim 30; Page 113; 139pp; English.

XX

CC The present peptide is a specific example corresp. to a highly generic
CC formula for ion channel forming peptides (ionophores). These ionophores
CC are known to have a broad range of potent antibiotic activity against
CC microorganisms including gram-positive and gram-negative bacteria, fungi,
CC viruses, protozoa and parasites. N-terminal modification (pref. mono-
CC subtn. by octanoyl) to produce an ion-channel forming peptide having a
CC lipophilic N-terminus increases the biological activity of the peptides
CC against target cells, viruses and virally-infected cells, compared to
CC peptides substd. with an acetyl group at the N-terminus. Compositions
CC comprising the peptides with lipophilic modifications are claimed for
CC inhibiting growth of a target cell, virus or virally-infected cell

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 1 KKK 3

RESULT 48

AAR90259

ID AAR90259 standard; peptide; 11 AA.

XX

AC AAR90259;

XX

DT 10-JUL-1996 (first entry)

XX

DE Ion-channel forming peptide #111 with lipophilic N-terminal group.

XX

KW Ion channel forming peptide; lipophilic; N-terminal modification;
KW magainin; inhibition; cell growth; viral replication; ionophore;
KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;
KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal amino group is mono- or di-substd. by
FT lipophilic moiety, esp. octanoyl"

XX

PN WO9519370-A1.

XX

PD 20-JUL-1995.

XX

PF 18-JAN-1995; 95WO-US000714.

XX

PR 18-JAN-1994; 94US-00184462.

XX

PA (MAGA-) MAGAININ PHARM INC.
XX
PI Kari U, Williams TJ, McLane M;
XX
DR WPI; 1995-263826/34.
XX
PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic
PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or
PT antitumour agents.
XX
PS Claim 25; Page 108; 139pp; English.
XX
CC The present peptide is a specific example corresp. to a highly generic
CC formula for ion channel forming peptides (ionophores). These ionophores
CC are known to have a broad range of potent antibiotic activity against
CC microorganisms including gram-positive and gram-negative bacteria, fungi,
CC viruses, protozoa and parasites. N-terminal modification (pref. mono-
CC substn. by octanoyl) to produce an ion-channel forming peptide having a
CC lipophilic N-terminus increases the biological activity of the peptides
CC against target cells, viruses and virally-infected cells, compared to
CC peptides substn. with an acetyl group at the N-terminus. Compositions
CC comprising the peptides with lipophilic modifications are claimed for
CC inhibiting growth of a target cell, virus or virally-infected cell
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 49
AAR91788
ID AAR91788 standard; peptide; 11 AA.
XX
AC AAR91788;
XX
DT 11-JUL-1996 (first entry)
XX
DE Ion-channel forming peptide #123 with lipophilic N-terminal group.
XX
KW Ion channel forming peptide; lipophilic; N-terminal modification;
KW magainin; inhibition; cell growth; viral replication; ionophore;
KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;
KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal amino group is mono-substd. by
FT octanoyl"
FT Modified-site 11

FT /note= "C-terminal amide"
XX
PN WO9519370-A1.
XX
PD 20-JUL-1995.
XX
PF 18-JAN-1995; 95WO-US000714.
XX
PR 18-JAN-1994; 94US-00184462.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Kari U, Williams TJ, McLane M;
XX
DR WPI; 1995-263826/34.
XX
PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic
PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or
PT antitumour agents.
XX
PS Example 1; Page 111; 139pp; English.
XX
CC Various ion channel forming peptides (ionophores) in C-terminal amide
CC form were modified by N-terminal substn. with a lipophilic group and then
CC tested for activity against S.aureus ATCC 25923 (S), P.aeruginosa ATCC
CC 27853 (P), E.coli ATCC 25922 (E) and C.albicans (C). Results indicated
CC that when a biologically active peptide is substn. with a lipophilic
CC moiety, the peptide has increased activity against a range of
CC microorganisms. Compositions comprising such peptides with lipophilic
CC modifications are claimed for inhibiting growth of a target cell, virus
CC or virally-infected cell. Minimum inhibitory concentrations (in
CC microgram/ml) for the present peptide against S, P, E and C,
CC respectively, were: 32, 16, 32 and 32
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 7 AKK 9

RESULT 50
AAR91787
ID AAR91787 standard; peptide; 11 AA.
XX
AC AAR91787;
XX
DT 11-JUL-1996 (first entry)
XX
DE Ion-channel forming peptide #122 with lipophilic N-terminal group.
XX
KW Ion channel forming peptide; lipophilic; N-terminal modification;
KW magainin; inhibition; cell growth; viral replication; ionophore;

KW membrane permeability; antimicrobial; anti-bacterial; antibiotic;
KW anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal amino group is mono-substd. by
FT octanoyl"
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN WO9519370-A1.
XX
PD 20-JUL-1995.
XX
PF 18-JAN-1995; 95WO-US000714.
XX
PR 18-JAN-1994; 94US-00184462.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Kari U, Williams TJ, McLane M;
XX
DR WPI; 1995-263826/34.
XX
PT Ion channel-forming amphiphilic peptide(s) with N-terminal lipophilic
PT gps. - useful e.g. as antiviral, antibacterial, antiparasitic or
PT antitumour agents.
XX
PS Example 1; Page 111; 139pp; English.
XX
CC Various ion channel forming peptides (ionophores) in C-terminal amide
CC form were modified by N-terminal subtn. with a lipophilic group and then
CC tested for activity against S.aureus ATCC 25923 (S), P.aeruginosa ATCC
CC 27853 (P), E.coli ATCC 25922 (E) and C.albicans (C). Results indicated
CC that when a biologically active peptide is substd. with a lipophilic
CC moiety, the peptide has increased activity against a range of
CC microorganisms. Compositions comprising such peptides with lipophilic
CC modifications are claimed for inhibiting growth of a target cell, virus
CC or virally-infected cell. Minimum inhibitory concentrations (in
CC microgram/ml) for the present peptide against S, P, E and C,
CC respectively, were: 32, 32, 64 and 64
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
Db 7 AKK 9

RESULT 51
AAR76755

ID AAR76755 standard; peptide; 11 AA.
XX
AC AAR76755;
XX
DT 18-MAR-1996 (first entry)
XX
DE E. coli FimH MFP class (+) binding peptide, sM5(175-184).
XX
KW FimH; type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue;
KW FimA; FimF; FimG; receptor binding site; MEP class; MF class; M class.
XX
OS Synthetic.
XX
PN WO9520657-A1.
XX
PD 03-AUG-1995.
XX
PF 27-JAN-1995; 95WO-DK000042.
XX
PR 27-JAN-1994; 94US-00187166.
XX
PA (GXBI-) GX BIOSYSTEMS AS.
XX
PI Sokurenko EV, Hasty DL, Klemm P, Pallesen L, Molin S;
XX
DR WPI; 1995-275442/36.
XX
PT Receptor specific bacterial adhesins - useful for targetting active
PT compounds and microbial cells to locations of receptors.
XX
PS Example 4; Page 67; 152pp; English.
XX
CC The sequences given in AAR76749-62 represent peptide fragments which were
CC used in adhesion assays with the FimH protein from E. coli strain CSH-50
CC to test the binding of the MFP class of FimH adhesins. Most forms of the
CC FimH adhesin target, and bind to, oligosaccharide structures containing
CC terminally located alpha-D-mannoside residues. FimH contains 4 cysteine
CC residues assumed to direct folding of the molecule into distinct
CC functional domains. For comparison FimA and the minor components FimF and
CC FimG only have 2 cysteine residues. The localisation of the cysteine
CC residues in FimH points to a tandem arrangement of two ancestral genes.
CC Similar amino acids can be found in similar positions in the two halves
CC of the FimH protein. The "midway" point is located roughly around residue
CC 150 in the mature protein. The two halves or domains of FimH have evolved
CC differently with the N-terminal section becoming the domain harbouring
CC the receptor binding site, whereas the C-terminal sector became the
CC domain of the molecule required for integration into the fimbrial
CC organelle. Variant FimH adhesins may be useful for targetting active
CC compounds and microbial cells to locations comprising selected receptors
CC to which the adhesins bind
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEQ 6
|||
Db 8 KEQ 10

RESULT 52

AAR66819

ID AAR66819 standard; peptide; 11 AA.

XX

AC AAR66819;

XX

DT 25-MAR-2003 (revised)

DT 11-SEP-1995 (first entry)

XX

DE Mouse syndecan-1 cytoplasmic fragment for probe design.

XX

KW Cell surface; proteoglycan; syndecan; mouse; mammary; epithelial cell;
KW ectodomain; NMuMG; glycosylation; heparan sulphate; chondroitin sulphate;
KW chimaera; chimaeric molecule; effector molecule; receptor; drug;
KW antibody; diagnostic agent.

XX

OS Synthetic.

XX

PN WO9500633-A2.

XX

PD 05-JAN-1995.

XX

PF 17-JUN-1994; 94WO-US006920.

XX

PR 17-JUN-1993; 93US-00078683.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX

PI Saunders S, Bernfield M, Kato M;

XX

DR WPI; 1995-052071/07.

DR N-PSDB; AAQ81751.

XX

PT DNA and protein sequences for recombinant syndecan-derived
PT proteoglycan(s) - comprising a core protein having glycosylation sites
PT for heparin sulphate glycosaminoglycan side chains.

XX

PS Claim 43; Page 88; 97pp; English.

XX

CC A peptide fragment from the cytoplasmic region of the mouse syndecan-1
CC proteoglycan, used to design oligonucleotide probes AAQ81751-2. The
CC probes can be used to detect and isolate homologs of the mouse syndecan-1
CC gene (AAQ81748) in closely related species or tissues. The functional
CC domains, esp. the soluble extracellular or heparan binding site, of the
CC syndecan molecules (see AAR66797-812) can be used to construct chimaeras
CC by linking them to biological effector molecules, cell surface receptors,
CC drugs, antibodies, diagnostic agents or components of microorganisms.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 4 KKK 6

RESULT 53

AAR98139

ID AAR98139 standard; peptide; 11 AA.

XX

AC AAR98139;

XX

DT 17-DEC-1996 (first entry)

XX

DE C-myc epitope recognised by mouse monoclonal antibody 9E10.

XX

KW sucrose transporter; primer; PCR; polymerase chain reaction; flowering;

KW early; increase number; induce.

XX

OS Synthetic.

XX

PN DE4439748-A1.

XX

PD 02-MAY-1996.

XX

PF 31-OCT-1994; 94DE-04439748.

XX

PR 31-OCT-1994; 94DE-04439748.

XX

PA (GENB-) INST GENBIOLOGISCHE FORSCHUNG.

XX

PI Leggewie G, Riesmeier J, Frommer W;

XX

DR WPI; 1996-231536/24.

XX

PT Using DNA encoding the sucrose transporter to alter flowering in plants -
PT esp. to induce earlier flowering and to increase number of flowers.

XX

PS Example 1; Page 7; 13pp; German.

XX

CC The present sequence is a c-Myc epitope recognised by the mouse
CC monoclonal antibody 9E10. It was added to the C-terminal end of spinach
CC sucrose transporter by using AAT30029. AAT30028-29 were used to amplify a
CC 1600 bp long DNA fragment (nucleotides 70-1644 of clone pS21 from
CC Reismeier et al. EMBO J. 11:4705-4713) encoding spinach sucrose
CC transporter. The resulting PCR product was cut with PstI and ligated with
CC PstI cleaved pUC18 and designated p-S21-Myc8. This plasmid was used to
CC construct p-omega-S21 which was used to transform tobacco plants by
CC Agrobacterium-mediated gene transfer. Transformed plants flowered about
CC 14 days earlier than the wild type and produced more flowers but fewer
CC leaves. Earlier flowering and increased number of flowers is due to
CC overexpression of the sucrose transporter

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 54

AAW09326

ID AAW09326 standard; peptide; 11 AA.

XX

AC AAW09326;

XX

DT 10-JUN-1997 (first entry)

XX

DE Myc epitope tag peptide.

XX

KW Chimaeric; bispecific; DNA binding domain; trans; activator; repressor;
KW diphtheria; Pseudomonas; toxin; thymidine kinase; single chain antibody;
KW pathogen; HIV Tat; papilloma virus; E6/E7; Epstein-Barr virus; EBNA;
KW hyperproliferation; p53; tumour; oligomerisation.

XX

OS Synthetic.

XX

PN WO9630512-A1.

XX

PD 03-OCT-1996.

XX

PF 29-MAR-1996; 96WO-FR000477.

XX

PR 31-MAR-1995; 95FR-00003841.

XX

PA (RHON) RHONE POULENC RORER SA.

XX

PI Bracco L, Schweighoffer F, Tocque B;

XX

DR WPI; 1996-455359/45.

DR N-PSDB; AAT48002.

XX

PT Conditional gene expression system triggered by e.g. infection or hyper-
PT proliferation - comprises novel bi:specific proteins having DNA-binding
PT domain and second domain specific for trans-activator or repressor, for
PT gene therapy.

XX

PS Disclosure; Page 12; 81pp; French.

XX

CC The invention relates to novel chimaeric, bispecific proteins which
CC comprise: (a) a DNA binding domain and (b) a domain which binds a trans-
CC activator (TA), trans-repressor (TR) or their complexes, which are
CC characteristic of a physiological or physiopathological state. The novel
CC chimaeric, bispecific proteins allow expression of a therapeutic protein
CC (e.g. diphtheria or Pseudomonas toxins, thymidine kinase, single chain
CC antibodies) to be regulated in response to particular conditions. The
CC chimearic protein may be fused to an epitope tag recognised by an

CC antibody for immunological detection of the chimearic protein. This is
CC the sequence of the myc epitope tag

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EQK 7
|||
Db 1 EQK 3

RESULT 55

AAW04041

ID AAW04041 standard; peptide; 11 AA.

XX

AC AAW04041;

XX

DT 01-NOV-1996 (first entry)

XX

DE Antifungal peptide XMP.350.

XX

KW Antifungal peptide; inhibitor; Domain III; polymorphonuclear leukocyte;
KW bactericidal/permeability-increasing protein; BPI; mammalian; PMN; fungi;
KW neutrophil; replication inhibitor; fungal infection; Aspergillus;
KW Cryptococcus; Candida; C.albicans; C.galabrat; C.krusei; C.lusitaniae;
KW C.parapsilosis; C.tropicalis; therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "amidated"

XX

PN WO9608509-A1.

XX

PD 21-MAR-1996.

XX

PF 20-JUL-1995; 95WO-US009262.

XX

PR 15-SEP-1994; 94US-00306473.

PR 13-JAN-1995; 95US-00372105.

XX

PA (XOMA) XOMA CORP.

XX

PI Little RG, Lim E, Fadem MB;

XX

DR WPI; 1996-179900/18.

XX

PT Antifungal peptide(s) derived from Domain III of BPI protein - used in
PT vitro for killing or inhibiting replication of fungi, esp. Candida
PT species.

XX

PS Claim 5; Page 163; 199pp; English.

XX

CC AAW04000-W04160 represent antifungal peptides. These sequences are based
CC on (or derived from) Domain III of the bactericidal/permeability-
CC increasing protein (BPI). BPI is a protein that can be isolated from the
CC granules of mammalian polymorphonuclear leukocytes (PMNs or neutrophils).
CC These antifungal peptides can be used for killing, or inhibiting
CC replication of, fungi in vitro. These sequences can also be used for
CC treatment of a fungal infection involving fungi from the species *Candida*,
CC *Aspergillus* and *Cryptococcus*. The sequences are especially useful for
CC treating *C.albicans*, *C.galabrat*, *C.krusei*, *C.lusitaniae*, *C.parapsilosis*
CC and *C.tropicalis* infections
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 1 KKK 3

RESULT 56

AAR92030

ID AAR92030 standard; peptide; 11 AA.

XX

AC AAR92030;

XX

DT 29-MAY-1996 (first entry)

XX

DE Hydrophilic peptide for epimorphin modification (2).

XX

KW Epimorphin; human; mouse; wound; burn; epithelial tissue; diagnosis;
KW treatment; morphogenetic abnormality; cosmetic; hair growth stimulator.

XX

OS Synthetic.

XX

PN EP698666-A2.

XX

PD 28-FEB-1996.

XX

PF 20-JUN-1995; 95EP-00304270.

XX

PR 21-JUN-1994; 94JP-00162874.

PR 31-MAR-1995; 95JP-00099979.

PR 31-MAR-1995; 95JP-00099980.

XX

PA (SUME) SUMITOMO ELECTRIC IND CO.

XX

PI Hirai Y, Koshida S, Oka Y;

XX

DR WPI; 1996-118213/13.

XX

PT Novel polypeptide containing an epimorphin functional domain - has
PT possible benefits in epithelial tissue treatments, e.g. burns and for
PT artificial organs.

XX

PS Claim 8; Page 57; 62pp; English.

XX

CC New polypeptides contain a first portion of 5-99 amino acids joined to a
CC second portion contg. at least a functional domain of epimorphin. The
CC first portion may be selected from the peptides given in AAR92029 to
CC AAR92036. The second portion may be full-length epimorphin (see AAR92037
CC to AAR92042 for human and mouse epimorphins). Fragments of epimorphins
CC given in AAT16083 to AAT16090 are used in the prodn. of modified
CC epimorphins. The modified epimorphins are useful for the development of
CC diagnosis and treatment of morphogenetic abnormalities of epithelial
CC tissue or novel remedies for wounds, eg burns, after surgery and for
CC artificial organs. They may also be used as components of cosmetics, hair
CC growth stimulators, etc

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 57

AAW01038

ID AAW01038 standard; peptide; 11 AA.

XX

AC AAW01038;

XX

DT 14-NOV-1996 (first entry)

XX

DE Myc epitope.

XX

KW hPAK65; serine kinase neoplasia; cancer; modulate; inhibit.

XX

OS Synthetic.

XX

PN US5518911-A.

XX

PD 21-MAY-1996.

XX

PF 06-JAN-1995; 95US-00369780.

XX

PR 06-JAN-1995; 95US-00369780.

XX

PA (ONYX-) ONYX PHARM INC.

XX

PI Martin GA, Abo A;

XX

DR WPI; 1996-259065/26.

XX

PT Human serine protein kinase p65 and related nucleic acid - useful in
PT screening modulators, potentially useful in treatment of cancer,
PT arthritis etc.

XX

PS Disclosure; Col 18; 41pp; English.

XX

CC The present sequence is that of a Myc-epitope (with an added methionine).
CC It can be fused to the N-terminal of a PAK polypeptide or fragment (e.g.
CC p21-protein activated serine kinase p65 protein, referred to as hPAK65).
CC An antibody specific for the specific Myc-epitope would allow isolation
CC and identification of the fusion protein. hPAK65 is useful for
CC identifying agents which modulate or inhibit its protein kinase activity,
CC p21-binding, p21-induced autophosphorylation and its p21-bound phosphate
CC release activity. Preferably the agents modulate the rac1- and CDC42Hs-
CC interacting properties of hPAK65, and are useful to treat neoplasia

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 58

AAW11753

ID AAW11753 standard; peptide; 11 AA.

XX

AC AAW11753;

XX

DT 04-NOV-1997 (first entry)

XX

DE T-cell receptor peptide V(beta)5.1 (49-59)F or V(beta)5.4 (49-59)F.

XX

KW T-cell receptor; TCR; V(beta)5.1; V(beta)5.4; multiple sclerosis;
KW rheumatoid arthritis; myasthenia gravis; encephalomyelitis; diabetes;
KW inflammatory bowel disease; systemic lupus erythematosus; thyroiditis;
KW therapy; diagnosis; vaccine.

XX

OS Synthetic.

XX

PN WO9640778-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US009423.

XX

PR 07-JUN-1995; 95US-00476405.

XX

PA (CONN-) CONNECTIVE THERAPEUTICS INC.

XX

PI Vandenbark AA;

XX

DR WPI; 1997-099923/09.

XX

PT T cell receptor peptide derived from V(beta)-5 family - useful for
PT treating e.g. multiple sclerosis, myasthenia gravis, diabetes, etc.

XX

PS Claim 9; Page 42; 54pp; English.

XX

CC This sequence is a synthetic peptide based on amino acid residues 49-59
CC of the V(beta)5.1 and V(beta)5.4 regions of human T cell receptor (TCR).
CC It is a specifically preferred peptide for use in a claimed method for
CC the treatment, prevention or suppression of a T-cell mediated disease
CC such as multiple sclerosis, rheumatoid arthritis, myasthenia gravis,
CC encephalomyelitis, thyroiditis, diabetes, inflammatory bowel disease or
CC systemic lupus erythematosus. Claimed TCR peptides (AAW11741-65) are
CC derived from the V(beta)5 family, or are functional derivatives of
CC V(beta)5 peptides

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QRN 10
 |||

Db 7 QRN 9

RESULT 59

AAW12383

ID AAW12383 standard; peptide; 11 AA.

XX

AC AAW12383;

XX

DT 18-JUN-1997 (first entry)

XX

DE Myc.1 epitope tag.

XX

KW Plasmid pPhOx.TM; eukaryotic expression vector; transfected cell;
KW single chain antibody; sFv; molecular hook; Myc.1 epitope tag.

XX

OS Synthetic.

XX

PN WO9708186-A1.

XX

PD 06-MAR-1997.

XX

PF 23-AUG-1996; 96WO-US015819.

XX

PR 24-AUG-1995; 95US-00518835.

XX

PA (INVI-) INVITROGEN CORP.

XX

PI Chesnut RD, Baytan A, Hoeffler JP, Bernhard A, Chang M;

XX

DR WPI; 1997-179169/16.

XX

PT Eukaryotic expression vector - for identification and separation of
PT transfected cells from total cell population.

XX

PS Example 1; Page 26; 83pp; English.

XX

CC A DNA fragment encompassing the nucleotides encoding amino acids 514-562
CC of the human platelet derived growth factor receptor was amplified using
CC primers that incorporated restriction sites and the Myc.1 epitope tag
CC (AAW12383) that is recognised by monoclonal antibody 9E10.2. This
CC fragment was cloned into the T/A cloning vector pCRII and utilised in the
CC construction of eukaryotic expression vector pPhOx.TM (see also
CC AAT63235). Expression of the Myc.1 tag allows detection of the encoded
CC single chain antibody by 9E10.2. Vector pPhOx.TM is used in novel methods
CC for the identification and isolation of transfected eukaryotic cells

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 60

AAW18499

ID AAW18499 standard; peptide; 11 AA.

XX

AC AAW18499;

XX

DT 19-FEB-1998 (first entry)

XX

DE Amino-terminal peptide 1 associated with novel helicase.

XX

KW Nucleic acid binding protein; helicase; leflunomide; assaying;
KW 4-(N-(4-trifluoromethylphenyl)-5-methyl-isoxazole; identification;
KW anticancer; antiatherosclerotic; immunosuppressant; sequencing;
KW antiinflammatory; antiviral; antifungal; antibacterial; treatment;
KW Alzheimer's disease; cancer; rheumatism; arthrosis; determination;
KW atherosclerosis; osteoporosis; acute infection; chronic infection;
KW autoimmune disease; diabetes; organ transplant; isolation;
KW amino-terminal.

XX

OS Homo sapiens.

XX

PN DE19545126-A1.

XX

PD 05-JUN-1997.

XX

PF 04-DEC-1995; 95DE-01045126.

XX

PR 04-DEC-1995; 95DE-01045126.

XX

PA (FARH) HOECHST AG.

XX

PI Kirschbaum B, Muellner S, Bartlett R;

XX

DR WPI; 1997-299388/28.

XX

PT New nucleic acid binding protein with helicase activity - is strongly

PT induced by leflunomide, used to isolate specific binding RNA and for
PT identifying substances with anticancer, antiviral etc. activities.
XX
PS Example 4; Page 15; 28pp; German.
XX
CC The present sequence is an amino-terminal peptide associated with a novel
CC nucleic acid binding protein with helicase activity, the mRNA of which
CC (or its translation products) is strongly expressed in presence of
CC leflunomide, i.e. 4-(N-(4-trifluoromethylphenyl)-5-methyl-isoxazole, or a
CC compound with similar activity. The helicase can be used in assay systems
CC to identify/discover anticancer, antiatherosclerotic, immunosuppressing,
CC antiinflammatory, antiviral, antifungal and antibacterial agents, e.g. to
CC treat Alzheimer's disease, cancer, rheumatism, arthrosis,
CC atherosclerosis, osteoporosis, acute/chronic infections, autoimmune
CC disease, diabetes and complications of organ transplants, and to isolate
CC or determine the sequences of specific binding RNA

XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
|||
Db 9 KKE 11

RESULT 61
AAW21913
ID AAW21913 standard; peptide; 11 AA.
XX
AC AAW21913;
XX
DT 14-JAN-1998 (first entry)
XX
DE Smooth muscle fibre proliferation inhibitor peptide 2.
XX
KW Generic; TFPI; inhibitor; proliferation; smooth muscle cell; prevention;
KW treatment; arteriosclerosis; restenosis; angioplasty; luminal stenosis;
KW vascular transplantation; leiomyosarcoma; human.
XX
OS Synthetic.
XX
PN WO9715598-A1.
XX
PD 01-MAY-1997.
XX
PF 23-OCT-1996; 96WO-JP003080.
XX
PR 24-OCT-1995; 95JP-00300792.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Nakahara Y, Hara S, Kamikubo Y, Takemoto S, Miyamoto S;
XX
DR WPI; 1997-258960/23.

XX
PT Peptide(s) comprising basic rich peptide bound at C-terminal to
PT consecutive hydrophobic rich peptide - useful for inhibiting smooth
PT muscle fibre cell proliferation.
XX
PS Example 3; Page 13; 45pp; Japanese.
XX
CC Novel peptides contain: (a) a peptide sequence (P1) rich in basic amino
CC acid residues (preferably lysine, arginine or histidine); and (b) a
CC peptide sequence (P2) containing at least two consecutive hydrophobic
CC amino acid residues (preferably phenylalanine, isoleucine, leucine,
CC methionine, proline, valine, tryptophan or tyrosine); where P2 is bound
CC to the C-terminal end of P1 either directly or through a linker sequence
CC of several amino acid residues. The peptides inhibit proliferation of
CC smooth muscle cells, and are useful in the prevention and treatment of
CC arteriosclerosis associated with smooth muscle cell proliferation,
CC restenosis after angioplasty, luminal stenosis after vascular
CC transplantation, and leiomyosarcoma. AAW21913-29 are specific inhibitory
CC peptides
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
|||
Db 8 KQR 10

RESULT 62
AAW09909
ID AAW09909 standard; peptide; 11 AA.
XX
AC AAW09909;
XX
DT 16-OCT-1997 (first entry)
XX
DE Prostate specific membrane antigen peptide PSM-P26.
XX
KW Prostate specific membrane antigen; PSMA; prostate specific antigen; PSA;
KW prostate cancer; adoptive cellular immunotherapy; therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO9704802-A1.
XX
PD 13-FEB-1997.
XX
PF 29-JUL-1996; 96WO-US012389.
XX
PR 31-JUL-1995; 95US-00509254.
XX
PA (PACI-) PACIFIC NORTHWEST CANCER FOUND.
XX
PI Murphy GP, Boynton AL, Tjoa BA;

XX
DR WPI; 1997-145375/13.
XX
PT Use of dendritic cells for prostate cancer immuno:therapy - the cells are exposed to prostate cancer antigen, then administered to the patient where they activate and proliferate T-cells.
XX
PS Claim 3; Page 47; 69pp; English.
XX
CC Peptide PSM-P26 (AAW09909) corresponds to amino acid residues 398-408 of prostate specific membrane antigen (PSMA). A method for producing a cancer growth inhibiting response comprises exposing human dendritic cells (DCs) to PSM-P26 or other PSMA or prostate specific antigen peptides (see also AAW09889-908 and AAW09910-26), and then administering the DCs to a prostate cancer patient to activate T cell responses in vivo. Alternatively, the T cell response is activated in vitro and the T cells are then administered to the patient. In either case, the DCs are used to elicit an immunotherapeutic growth inhibiting response against a primary or metastatic prostate tumour. PSM-P26 was selected to be presented by DCs to activate T cells of a patient which match the A11 haplotype
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
|||
Db 9 KKE 11

RESULT 63
AAW44580
ID AAW44580 standard; peptide; 11 AA.
XX
AC AAW44580;
XX
DT 27-APR-1998 (first entry)
XX
DE Anti-fungal peptide #181 based on BPI protein (residues 142-169).
XX
KW Anti-fungal peptide; bactericidal-permeability-increasing protein; BPI;
KW polymorphonuclear leukocyte; fungicide.
XX
OS Synthetic.
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN WO9704008-A1.
XX
PD 06-FEB-1997.
XX

PF 21-MAR-1996; 96WO-US003845.
XX
PR 20-JUL-1995; 95US-00504841.
XX
PA (XOMA) XOMA CORP.
XX
PI Little RG, Lim E, Fadem MB;
XX
DR WPI; 1997-132578/12.
XX
PT Anti-fungal peptide(s) derived from or based on domain III of
PT bactericidal-permeability-increasing protein - are used in vitro or in
PT vivo as a fungicides.

XX
PS Claim 1; Page 200; 230pp; English.
XX
CC This is a specifically claimed anti-fungal peptide which is based on
CC domain III (amino acids 142-160) of bactericidal-permeability-increasing
CC protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC leukocytes. It is used in compositions with diluents, carriers or
CC adjuvants to treat fungal infections in patients. It may also be used in
CC vitro to kill or inhibit the replication of fungi, such as in
CC decontaminating fluids and sterilising medical and implant devices
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 1 KKK 3

RESULT 64
AAW38865
ID AAW38865 standard; peptide; 11 AA.
XX
AC AAW38865;
XX
DT 30-MAR-1998 (first entry)
XX
DE Delivery peptide used in peptide macromolecule complex.
XX
KW Delivery peptide; peptide-macromolecule complex; macromolecule delivery;
KW non-exchangeable lipophilic peptide; disease therapy; cell targeting.
XX
OS Synthetic.
XX
PN WO9725070-A2.
XX
PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-US000454.
XX
PR 08-JAN-1996; 96US-00584043.

XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Smith LC, Sparrow JT, Hauer J, Mims MP;
XX
DR WPI; 1997-372622/34.
XX
PT New lipophilic peptide-macromolecule complexes - used for the delivery of
PT macromolecules to cells, particularly for gene therapy.
XX
PS Disclosure; Page 51; 106pp; English.
XX
CC This sequence represents a delivery peptide that can be used in the
CC peptide-macromolecule complex of the invention. The peptide-macromolecule
CC complex of the invention is for delivering a macromolecule into a cell,
CC and comprises a non-exchangeable lipophilic peptide (LP) comprising a
CC delivery peptide associated with a lipid moiety, where the delivery
CC peptide portion of the LP is complexed to the macromolecule. The
CC complexes can be used for the delivery of macromolecules such as nucleic
CC acids, proteins, oligonucleotides, lipids or carbohydrates. They can be
CC used to treat diseases by enhancing delivery of specific nucleic acid to
CC the appropriate targeted cells. They can also be used to create
CC transformed cells as well as transgenic animals for assessing human
CC disease in an animal model. They can also be used for livestock
CC agricultural purposes. The complex is capable of transporting the
CC macromolecule in a stable and condensed state and releasing the molecule
CC into the cellular interior. The complex can bind with a cell surface
CC receptor, lyse an endosome and target the nucleus of the cell
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 1 KKK 3

RESULT 65
AAW38785
ID AAW38785 standard; peptide; 11 AA.
XX
AC AAW38785;
XX
DT 30-MAR-1998 (first entry)
XX
DE Delivery peptide used in peptide macromolecule complex.
XX
KW Delivery peptide; peptide-macromolecule complex; macromolecule delivery;
KW non-exchangeable lipophilic peptide; disease therapy; cell targeting.
XX
OS Synthetic.
XX
PN WO9725070-A2.
XX

PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-US000454.
XX
PR 08-JAN-1996; 96US-00584043.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Smith LC, Sparrow JT, Hauer J, Mims MP;
XX
DR WPI; 1997-372622/34.
XX
PT New lipophilic peptide-macromolecule complexes - used for the delivery of
PT macromolecules to cells, particularly for gene therapy.
XX
PS Claim 6; Page 83; 106pp; English.
XX
CC This sequence represents a delivery peptide that can be used in the
CC peptide-macromolecule complex of the invention. The peptide-macromolecule
CC complex of the invention is for delivering a macromolecule into a cell,
CC and comprises a non-exchangeable lipophilic peptide (LP) comprising a
CC delivery peptide associated with a lipid moiety, where the delivery
CC peptide portion of the LP is complexed to the macromolecule. The
CC complexes can be used for the delivery of macromolecules such as nucleic
CC acids, proteins, oligonucleotides, lipids or carbohydrates. They can be
CC used to treat diseases by enhancing delivery of specific nucleic acid to
CC the appropriate targeted cells. They can also be used to create
CC transformed cells as well as transgenic animals for assessing human
CC disease in an animal model. They can also be used for livestock
CC agricultural purposes. The complex is capable of transporting the
CC macromolecule in a stable and condensed state and releasing the molecule
CC into the cellular interior. The complex can bind with a cell surface
CC receptor, lyse an endosome and target the nucleus of the cell
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 1 KKK 3

RESULT 66
AAW38822
ID AAW38822 standard; peptide; 11 AA.
XX
AC AAW38822;
XX
DT 30-MAR-1998 (first entry)
XX
DE Delivery peptide used in peptide macromolecule complex.
XX
KW Delivery peptide; peptide-macromolecule complex; macromolecule delivery;
KW non-exchangeable lipophilic peptide; disease therapy; cell targeting.

XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 10
FT /note= "any amino acid"
XX
PN WO9725070-A2.
XX
PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-US000454.
XX
PR 08-JAN-1996; 96US-00584043.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Smith LC, Sparrow JT, Hauer J, Mims MP;
XX
DR WPI; 1997-372622/34.
XX
PT New lipophilic peptide-macromolecule complexes - used for the delivery of
PT macromolecules to cells, particularly for gene therapy.
XX
PS Claim 6; Page 63; 106pp; English.
XX
CC This sequence represents a delivery peptide that can be used in the
CC peptide-macromolecule complex of the invention. The peptide-macromolecule
CC complex of the invention is for delivering a macromolecule into a cell,
CC and comprises a non-exchangeable lipophilic peptide (LP) comprising a
CC delivery peptide associated with a lipid moiety, where the delivery
CC peptide portion of the LP is complexed to the macromolecule. The
CC complexes can be used for the delivery of macromolecules such as nucleic
CC acids, proteins, oligonucleotides, lipids or carbohydrates. They can be
CC used to treat diseases by enhancing delivery of specific nucleic acid to
CC the appropriate targeted cells. They can also be used to create
CC transformed cells as well as transgenic animals for assessing human
CC disease in an animal model. They can also be used for livestock
CC agricultural purposes. The complex is capable of transporting the
CC macromolecule in a stable and condensed state and releasing the molecule
CC into the cellular interior. The complex can bind with a cell surface
CC receptor, lyse an endosome and target the nucleus of the cell
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 1 KKK 3

RESULT 67
AAW26074
ID AAW26074 standard; peptide; 11 AA.

XX
AC AAW26074;
XX
DT 28-OCT-1997 (first entry)
XX
DE M32 derivative of tenecin peptide fragment TED.
XX
KW Tenecin; antibiotic; antifungal peptide; *Tenebrio molitor*; chemotherapy;
KW systemic infection; pathogen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "amidated"
XX
PN WO9702286-A1.
XX
PD 23-JAN-1997.
XX
PF 11-MAR-1996; 96WO-KR000034.
XX
PR 06-JUL-1995; 95KR-00019694.
PR 29-JAN-1996; 96KR-00001909.
PR 29-JAN-1996; 96KR-00001910.
PR 29-JAN-1996; 96KR-00001911.
XX
PA (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
XX
PI Lee K, Hong S, Cho H, Lee B, Chung K, Yoon J, Oh J, Moon H;
XX
DR WPI; 1997-108913/10.
XX
PT Acid- or amide-form peptide(s) with antibacterial and antifungal activity
PT - used for chemotherapy of local and systemic infections caused by
PT pathogenic bacteria.
XX
PS Example 4; Page 17; 30pp; English.
XX
CC AAW26002-W26077 represent derivatives of the antibiotic fragments of
CC tenecin (see AAW26000) shown in AAW01830-W10835. AAW01830-W01835 are
CC amidated derivatives of antibiotic fragments of the wild type tenecin
CC sequence. These sequences are used as the antibacterial and antifungal
CC peptides of the invention. Tenecin is an antibacterial peptide isolated
CC from *Tenebrio molitor* larvae. Tenecin does have some drawbacks which
CC prevent it from practical use. Tenecin has a narrow spectrum of target
CC cells, and due to its large molecular size may provoke antigen-antibody
CC reactions in vivo, and is also unstable. The peptides can be used for the
CC development of antibacterial and antifungal agents for the chemotherapy
CC of local and systemic infections caused by pathogenic bacteria and/or
CC fungi and can be formulated into potent antibacterial and/or fungal
CC agents. The peptides have superior antibacterial and/or antifungal
CC activity, while causing no cytotoxicity. They do not give rise to lysing
CC of red blood cells. These peptides also have improved stability over the
CC wild type tenecin
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 1 KKK 3

RESULT 68

AAW16616

ID AAW16616 standard; peptide; 11 AA.

XX

AC AAW16616;

XX

DT 19-DEC-1997 (first entry)

XX

DE Phosphoinositide-3 kinase p110alpha conserved motif.

XX

KW Phosphoinositide 3 kinase; PI-3 kinase; wortmannin.

XX

OS Synthetic.

XX

PN WO9715658-A1.

XX

PD 01-MAY-1997.

XX

PF 28-OCT-1996; 96WO-GB002614.

XX

PR 26-OCT-1995; 95GB-00021987.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Wymann MP, Bulgarelli-Vela G, Panayotou G, Vanhaesebroeck B;

PI Zvelebil MJ, Waterfield MD;

XX

DR WPI; 1997-259013/23.

XX

PT Phospho:inositide 3 kinase wortmannin interaction site - to identify and
PT design ligands which regulate phospho:inositide 3 kinase activity.

XX

PS Disclosure; Page 32; 71pp; English.

XX

CC A novel interaction site has been discovered on phosphoinositide 3 (PI-3)
CC kinase, or a homologue or analogue. The interaction site modulates the
CC activity of PI-3 kinase when exposed to a modulator, and has a molecular
CC shape adapted to interact with at least a part of the modulator so as to
CC modulate PI-3 kinase activity. The present sequence represents a
CC conserved motif (resembling K(X)nKKK where n=3-7) in PI-3 kinase
CC p110alpha, that was found to bind phosphatidylinositol in gelsolin and so
CC might constitute a binding site for the 4,5-phosphates of the lipid. The
CC activity of PI-3 kinase can be regulated by altering, e.g. substituting a
CC different amino acid or deleting any of the features of the site. The
CC site may be used to identify or design novel ligands which regulate the
CC activity of PI-3 kinase by generating a molecular model of the wortmannin
CC inhibition site of PI-3 kinase, identifying or designing ligands which

CC interact with at least part of the site and optionally contacting the
CC putative ligand with PI-3 kinase and monitoring PI-3 kinase activity

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4
|||
Db 1 KKK 3

RESULT 69

AAW19819

ID AAW19819 standard; peptide; 11 AA.

XX

AC AAW19819;

XX

DT 26-JAN-1998 (first entry)

XX

DE Universal transfer vector sequence of chimeric coat protein.

XX

KW Adenovirus; vector; coat protein; gene therapy; gene transfer; human;

KW cancer; autoimmune disease; heart disease; infection;

KW universal transfer vector; p193NS F5F2K(RKKK)2.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 2..9

FT /note= "heparin binding domain"

XX

PN WO9720051-A2.

XX

PD 05-JUN-1997.

XX

PF 27-NOV-1996; 96WO-US019150.

XX

PR 28-NOV-1995; 95US-00563368.

PR 21-AUG-1996; 96US-00700846.

PR 21-AUG-1996; 96US-00701124.

XX

PA (GENV-) GENVEC INC.

XX

PI Wickham TJ, Kovesdi I, Brough DE;

XX

DR WPI; 1997-310606/28.

DR N-PSDB; AAT70273.

XX

PT Adenoviral vectors containing chimeric coat protein - bind and enter
PT cells more efficiently, useful for gene therapy of e.g. cancer,

PT auto:immune diseases, etc.

XX

PS Claim 7; Page 61; 121pp; English.

XX

CC This peptide can be used as a universal transfer vector (UTV) and/or
CC spacer sequence in novel chimeric adenovirus coat proteins (CPs). The
CC peptide is encoded by a gene fragment (see AAT70273) of claimed transfer
CC plasmid p193NS F5F2K(RKKK)2. It includes a heparin binding domain and is
CC inserted into the adenoviral fibre loop. Claimed UTVs/spacers are given
CC in AAW19810-11, AAW19813-25, AAW19827, AAW19829, AAW19831-32 and AAW19834
CC -43). Claimed CPs, such as fibre proteins, differ from wild-type CPs by
CC the introduction of the UTV and/or spacer sequence e.g. in the fibre
CC loop. This imparts on the chimeric CP the ability to bind to and enter
CC cells by means of a novel cell surface binding site. Adenoviral vectors
CC comprising the chimeric CP are able to enter cells more efficiently than
CC vectors comprising wild-type CP, especially at lower m.o.i. They are
CC especially useful for gene therapy of e.g. cancers, genetic disorders,
CC pathogenic infections, heart disease or autoimmune diseases

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 3 KKK 5

RESULT 70

AAW43762

ID AAW43762 standard; peptide; 11 AA.

XX

AC AAW43762;

XX

DT 20-APR-1998 (first entry)

XX

DE Bactericidal/permeability increasing peptide XMP.350.

XX

KW Bactericidal/permeability increasing peptide; BPI; fusion protein;
KW bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
KW fungicidal; recombinant DNA; vector.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "Amidated"

XX

PN WO9735009-A1.

XX

PD 25-SEP-1997.

XX

PF 18-MAR-1997; 97WO-US005287.

XX

PR 22-MAR-1996; 96US-00621803.

XX

PA (XOMA) XOMA CORP.

XX

PI Better MD;

XX

DR WPI; 1997-480215/44.

XX

PT Recombinant production of bactericidal/permeability increasing protein -
PT by expression as a fusion protein in microbial host cells, then cleaving
PT the BPI peptide from the carrier.

XX

PS Claim 10; Page 130; 186pp; English.

XX

CC A new recombinant DNA vector construct has been developed which encodes a
CC fusion protein and is suitable for introduction into a bacterial host.
CC The vector comprises: (a) DNA encoding at least one cationic
CC bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
CC carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
CC located between (a) and (b). The present sequence represents a
CC specifically claimed BPI peptide. The peptides have many uses including
CC the treatment of bacterial and fungal infections. BPI peptides also bind
CC to endotoxins and heparin, neutralising their effects. The peptides have
CC further been shown to inhibit angiogenesis (partly due to heparin-binding
CC activity). The fusion proteins have been found to be expressed in large
CC amounts without significant proteolysis, and in some cases are actually
CC secreted from the host cells. This allows the indirect production of anti
CC -microbial BPI peptides in microbial hosts

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4

|||

Db 1 KKK 3

RESULT 71

AAW26548

ID AAW26548 standard; peptide; 11 AA.

XX

AC AAW26548;

XX

DT 16-JAN-1998 (first entry)

XX

DE Epithelial protein (precancer marker) peptide.

XX

KW Epithelial protein; heterogeneous nuclear ribonuclear protein;

KW 703D4 antigen; hnRNP-A2; hnRNP-B1; lung cancer; liver cancer;

KW renal cancer; prostate cancer; melanoma; head cancer; neck cancer;

KW myeloma; marker; carcinogenesis; diagnosis; human.

XX

OS Homo sapiens.

XX

PN WO9712975-A1.

XX

PD 10-APR-1997.

XX

PF 02-OCT-1996; 96WO-US015825.
XX
PR 02-OCT-1995; 95US-00538711.
PR 02-OCT-1996; 96US-00725027.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Mulshine JL, Tockman MS;
XX
DR WPI; 1997-226219/20.
XX
PT A new purified protein from epithelial cells - is expressed in high
PT amounts in cancer and pre:cancer cells; used as a marker for diagnosis
PT and treatment of cancer.
XX
PS Claim 2; Page 138; 171pp; English.
XX
CC 6 Claimed peptides (AAW26546-51) are CNBr fragments of an epithelial
CC protein, the antigen for monoclonal antibody 703D4, whose increased
CC presence in an epithelial cell is indicative of precancer, especially
CC lung cancer. The major epithelial protein was purified from human lung
CC cancer lines NCI-H720 and NCI-H157. It shares some sequence homology with
CC the heterogeneous nuclear ribonucleoprotein (hnRNP) A2 (see AAW26553). A
CC minor-copurifying epithelial protein shares some sequence homology with
CC the splice variant hnRNP-B1 (see AAW26552). The epithelial protein is a
CC marker of epithelial transformation in lung, breast, bone, ovary,
CC prostate, kidney, melanoma and myeloma, and may be causal in the process
CC of carcinogenesis. Methods are provided for monitoring the expression of
CC the epithelial protein, peptides and variants using molecular and
CC immunological techniques as a screen for (pre)cancer. A method of
CC computerised diagnosis of (pre)cancer is claimed that detects levels of
CC hnRNP mRNA. Also claimed are expression vectors, host cells and nucleic
CC acid probes and primers useful in diagnostic screens for lung, renal,
CC breast or prostate cancer, myeloma and melanoma
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEQ 6
|||
Db 3 KEQ 5

RESULT 72
AAW76269
ID AAW76269 standard; peptide; 11 AA.
XX
AC AAW76269;
XX
DT 11-JAN-1999 (first entry)
XX
DE Human calreticulin N-terminal peptide.
XX

KW Cell surface protein; vaccine; calcireticulin; human; sperm;
KW contraceptive; infertility.
XX
OS Homo sapiens.
XX
PN WO9836771-A1.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US002913.
XX
PR 25-FEB-1997; 97US-00806147.
XX
PA (UYVI-) UNIV VIRGINIA PATENT FOUND.
XX
PI Herr JC, Naaby-Hansen S, Flickinger CJ;
XX
DR WPI; 1998-480778/41.
XX
PT Analysing surface membrane proteins from e.g. viruses, bacteria or sperm
PT cells - useful for detecting infections or in the manufacture of
PT contraceptives.
XX
PS Example 13; Page 62; 155pp; English.
XX
CC This is an N-terminal peptide of human calcireticulin. It has been
CC identified as the N-terminal sequence of a 63 kDa, pI 4.3 human sperm
CC protein that was separated from other sperm proteins using lysis buffer
CC and preparative 2-D gel electrophoresis. Degenerate oligonucleotides (see
CC AAV56977-78) and an optimised oligonucleotide (see AAV56982) based on the
CC amino acid sequence of the N-terminal peptide have been utilised in the
CC RT-PCR cloning of human calcireticulin cDNA (see AAV56984). The invention
CC relates to a method for identifying the repertoire of proteins exposed on
CC the surface of a virus, bacterium or cell, and for the preparation of
CC vaccines thereto. The method involves vectorially labelling proteins on
CC the membrane surface, isolating the labelled membrane surface proteins by
CC 2-D gel electrophoresis and sequencing them. Methods are also provided of
CC detecting infertility and of producing contraceptives
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 KEQ 6
|||
Db 7 KEQ 9

RESULT 73
AAW50917
ID AAW50917 standard; peptide; 11 AA.
XX
AC AAW50917;
XX
DT 09-SEP-1998 (first entry)

XX
DE Amino acid sequence of a human epithelial peptide.
XX
KW Human epithelial peptide; marker; cancer; probe; hybridisation; primer;
KW amplification; lung; liver; kidney; breast; prostate; melanoma; myeloma;
KW antibody.
XX
OS Homo sapiens.
XX
PN WO9814469-A2.
XX
PD 09-APR-1998.
XX
PF 02-OCT-1997; 97WO-US017714.
XX
PR 02-OCT-1996; 96US-00725027.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Mulshine JL, Tockman MS;
XX
DR WPI; 1998-240016/21.
XX
PT New isolated epithelial protein as early marker of cancer - useful in
PT computer-assisted methods of diagnosis based on discriminant analysis of
PT optical images of cells.
XX
PS Claim 2; Page 10; 159pp; English.
XX
CC This is the amino acid sequence of the human epithelial peptide, used in
CC the method of the invention as early markers for cancer. Probes and
CC primers that hybridise to or amplify these peptides are used to diagnose
CC precancerous states, e.g. of lung, liver, kidney, breast, prostate, head
CC or neck, melanoma or myeloma, or to determine susceptibility to these
CC conditions and for monitoring treatment. Precancer is also indicated by
CC detecting post-translational modification of the epithelial peptide which
CC is a marker of epithelial cell transformation. Antibodies are potentially
CC useful for diagnosis and treatment of cancer
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEQ 6
|||
Db 3 KEQ 5

RESULT 74
AAW65554
ID AAW65554 standard; peptide; 11 AA.
XX
AC AAW65554;
XX

DT 15-OCT-1998 (first entry)
XX
DE Multiply branched peptide construct.
XX
KW Human immunodeficiency virus; envelope transmembrane glycoprotein; HIV;
KW multiple branch peptide construction; polylysine core; receptor affinity;
KW virostatic; MBPC; multiply branched peptide construct.
XX
OS Synthetic.
OS Human immunodeficiency virus.
XX
FH Key Location/Qualifiers
FT Peptide 1. .7
FT /label= peptide_derived_from_gp41_of_HIV
FT /note= "attached to the polylysine core via the alpha
FT amino group of Lys(8); a second copy of the 7-mer is
FT linked to Lys(8) via the omega amino group"
FT Modified-site 8
FT /note= "Lys(8) is linked to one copy of the gp41-derived
FT peptide of HIV through the alpha amino group, and two a
FT second copy of the peptide (not shown) via the omega
FT group"
FT Modified-site 9
FT /note= "the alpha amino group of of Lys(9) forms a
FT peptide linkage with the carboxyl group of Lys(8); the
FT omega amino group of Lys(9) forms a peptide bond with a
FT second Lys residue analogous to Lys(8)"
FT Modified-site 10
FT /note= "the alpha amimo group of Lys(10) forms a peptide
FT linkage with the carboxyl amino group of Lys(9); the
FT omega amino group of Lys(10) forms a peptide bond with a
FT second Lys residue analagous to Lys(9)"
FT Modified-site 11
FT /label= bAla
XX
PN WO9829443-A1.
XX
PD 09-JUL-1998.
XX
PF 30-DEC-1997; 97WO-EP007334.
XX
PR 31-DEC-1996; 96GB-00027114.
XX
PA (ARME-) ARMEL SA.
XX
PI Mabrouk K, Sabatier J, Rochat H, Van Rietschoten J;
XX
DR WPI; 1998-388041/33.
XX
PT New multiply branched peptide construct - comprises core matrix and many
PT gp41-derived peptide(s) attached, useful for, e.g. treating human immune
PT deficiency virus infection.
XX
PS Disclosure; Page 3; 15pp; English.
XX
CC The invention relates to multiply branched peptide constructs which
CC comprise a core matrix having bonded to it 2-16 peptides each containing

CC the present (RQGY) sequence, preceded by 0-4 amino acids and followed by
CC 2-4 amino acids. The multiply branched peptide constructs are used to
CC treat human immune deficiency virus (HIV) infection (they interfere with
CC HIV-mediated cell fusion). Since the core matrix is hidden by attached
CC peptides, the multiply branched peptide construct is not antigenic. The
CC present sequence represents a multiply branched peptide construct

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4

|||

Db 8 KKK 10

RESULT 75

AAW61490

ID AAW61490 standard; peptide; 11 AA.

XX

AC AAW61490;

XX

DT 12-OCT-1998 (first entry)

XX

DE Nuclear localisation signal protein.

XX

KW IL-10; IL-12; gamma interferon; nitric oxide synthase; asthma.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

/note= "Encoded by tc"

FT Misc-difference 10. .11

/note= "Encoded by complementary strand"

XX

PN WO9826066-A1.

XX

PD 18-JUN-1998.

XX

PF 09-DEC-1997; 97WO-US022454.

XX

PR 09-DEC-1996; 96US-0032260P.

XX

PA (ARIA-) ARIAD GENE THERAPEUTICS INC.

XX

PI Cerasoli F;

XX

DR WPI; 1998-348525/30.

DR N-PSDB; AAV45032.

XX

PT New method for treating or preventing asthma - comprises use of DNA
PT encoding IFN-gamma, IL-10, IL-12 or nitric oxide synthase and DNA for
PT control of expression using a ligand.

XX

PS Example 6; Page 28; 63pp; English.

XX

CC The nuclear localisation signal is inserted into the generic start site
CC which forms part of a chimeric protein. The chimeric protein is used in a
CC regulated expression system to permit the expression of a target gene
CC encoding IL-10, IL-12, gamma interferon or a nitric oxide synthase. This
CC can be used to target expression of the proteins in genetically
CC engineered cells within a mammal, preferably within cells of the mammals
CC airways. This can be used in the treatment and prevention of asthma and
CC related disorders

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

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Job time : 45.3077 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds
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Title: US-09-787-443A-20

Perfect score: 11

Sequence: 1 AKKKEQKQRNA 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4	36.4	11	4	US-09-025-596-34	Sequence 34, Appl
3	4	36.4	11	4	US-09-579-664B-33	Sequence 33, Appl
4	3	27.3	11	1	US-07-718-274A-31	Sequence 31, Appl
5	3	27.3	11	1	US-08-149-106-31	Sequence 31, Appl
6	3	27.3	11	1	US-07-851-941-14	Sequence 14, Appl
7	3	27.3	11	1	US-07-694-983-15	Sequence 15, Appl
8	3	27.3	11	1	US-08-193-521-18	Sequence 18, Appl
9	3	27.3	11	1	US-08-176-500-6	Sequence 6, Appl
10	3	27.3	11	1	US-08-298-021-31	Sequence 31, Appl
11	3	27.3	11	1	US-08-116-733-32	Sequence 32, Appl

12	3	27.3	11	1	US-08-116-733-39	Sequence 39, Appl
13	3	27.3	11	1	US-08-178-570-75	Sequence 75, Appl
14	3	27.3	11	1	US-08-471-052A-6	Sequence 6, Appl
15	3	27.3	11	1	US-08-434-120-112	Sequence 112, App
16	3	27.3	11	1	US-08-465-325-111	Sequence 111, App
17	3	27.3	11	1	US-08-465-325-122	Sequence 122, App
18	3	27.3	11	1	US-08-465-325-123	Sequence 123, App
19	3	27.3	11	1	US-08-465-325-128	Sequence 128, App
20	3	27.3	11	1	US-08-416-035-8	Sequence 8, Appl
21	3	27.3	11	1	US-08-189-331-6	Sequence 6, Appl
22	3	27.3	11	1	US-08-082-269D-2	Sequence 2, Appl
23	3	27.3	11	1	US-07-803-623B-20	Sequence 20, Appl
24	3	27.3	11	1	US-08-476-405A-14	Sequence 14, Appl
25	3	27.3	11	1	US-08-660-626-12	Sequence 12, Appl
26	3	27.3	11	2	US-08-478-386A-59	Sequence 59, Appl
27	3	27.3	11	2	US-08-292-597-59	Sequence 59, Appl
28	3	27.3	11	2	US-08-967-101-183	Sequence 183, App
29	3	27.3	11	2	US-08-806-084-20	Sequence 20, Appl
30	3	27.3	11	2	US-08-471-939-6	Sequence 6, Appl
31	3	27.3	11	2	US-08-701-124-19	Sequence 19, Appl
32	3	27.3	11	2	US-08-621-803-206	Sequence 206, App
33	3	27.3	11	2	US-08-471-800-6	Sequence 6, Appl
34	3	27.3	11	2	US-08-621-259A-181	Sequence 181, App
35	3	27.3	11	2	US-08-002-324-5	Sequence 5, Appl
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44	3	27.3	11	2	US-08-538-711A-3	Sequence 3, Appl
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49	3	27.3	11	3	US-09-087-716-59	Sequence 59, Appl
50	3	27.3	11	3	US-09-139-762A-124	Sequence 124, App
51	3	27.3	11	3	US-08-518-835-4	Sequence 4, Appl
52	3	27.3	11	3	US-08-970-833-8	Sequence 8, Appl
53	3	27.3	11	3	US-08-836-337-3	Sequence 3, Appl
54	3	27.3	11	3	US-09-015-003-5	Sequence 5, Appl
55	3	27.3	11	3	US-08-159-339A-1148	Sequence 1148, Ap
56	3	27.3	11	3	US-09-157-753-59	Sequence 59, Appl
57	3	27.3	11	3	US-09-157-230-59	Sequence 59, Appl
58	3	27.3	11	3	US-09-087-811-59	Sequence 59, Appl
59	3	27.3	11	3	US-09-130-225-19	Sequence 19, Appl
60	3	27.3	11	3	US-08-968-747-8	Sequence 8, Appl
61	3	27.3	11	3	US-09-156-855-59	Sequence 59, Appl
62	3	27.3	11	3	US-09-188-579-65	Sequence 65, Appl
63	3	27.3	11	3	US-09-212-971-17	Sequence 17, Appl
64	3	27.3	11	3	US-08-971-692-37	Sequence 37, Appl
65	3	27.3	11	3	US-09-124-698-183	Sequence 183, App
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67	3	27.3	11	3	US-08-493-071-22	Sequence 22, Appl
68	3	27.3	11	3	US-08-800-929A-17	Sequence 17, Appl

69	3	27.3	11	3	US-09-158-010-59	Sequence 59, Appl
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73	3	27.3	11	3	US-09-087-647-59	Sequence 59, Appl
74	3	27.3	11	3	US-08-114-877A-9	Sequence 9, Appli
75	3	27.3	11	3	US-08-114-877A-14	Sequence 14, Appl
76	3	27.3	11	3	US-08-602-999A-105	Sequence 105, App
77	3	27.3	11	3	US-09-051-986-2	Sequence 2, Appli
78	3	27.3	11	3	US-09-127-480-183	Sequence 183, App
79	3	27.3	11	3	US-08-659-254-8	Sequence 8, Appli
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83	3	27.3	11	3	US-08-725-027-3	Sequence 3, Appli
84	3	27.3	11	3	US-09-410-025-6	Sequence 6, Appli
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86	3	27.3	11	3	US-09-133-062D-28	Sequence 28, Appl
87	3	27.3	11	3	US-09-133-062D-29	Sequence 29, Appl
88	3	27.3	11	3	US-08-226-376-1	Sequence 1, Appli
89	3	27.3	11	3	US-09-217-352-206	Sequence 206, App
90	3	27.3	11	4	US-09-025-769B-275	Sequence 275, App
91	3	27.3	11	4	US-09-617-053A-17	Sequence 17, Appl
92	3	27.3	11	4	US-08-278-865-105	Sequence 105, App
93	3	27.3	11	4	US-09-201-970A-20	Sequence 20, Appl
94	3	27.3	11	4	US-09-302-629-59	Sequence 59, Appl
95	3	27.3	11	4	US-09-455-061-19	Sequence 19, Appl
96	3	27.3	11	4	US-08-584-043A-5	Sequence 5, Appli
97	3	27.3	11	4	US-08-584-043A-43	Sequence 43, Appl
98	3	27.3	11	4	US-08-584-043A-99	Sequence 99, Appl
99	3	27.3	11	4	US-09-115-737-111	Sequence 111, App
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ALIGNMENTS

RESULT 1

US-08-160-604-6

; Sequence 6, Application US/08160604

; Patent No. 6232522

; GENERAL INFORMATION:

; APPLICANT: Harley, John

; APPLICANT: James, Judith A.

; APPLICANT: Scofield, R. H.

; TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY

; NUMBER OF SEQUENCES: 127

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 1100 Peachtree Street, Suite 2800

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30309-4530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,604
; FILING DATE: 30-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867,819
; FILING DATE: 13-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,205
; FILING DATE: 31-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,947
; FILING DATE: 31-JAN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF114CIP(3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-160-604-6

Query Match 36.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEQK 7
 ||||
Db 5 KEQK 8

RESULT 2
US-09-025-596-34
; Sequence 34, Application US/09025596
; Patent No. 6340463
; GENERAL INFORMATION:
; APPLICANT: Mitchell, William M.
; APPLICANT: Stratton, Charles W.
; TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: VDB98-01
; CURRENT APPLICATION NUMBER: US/09/025,596
; CURRENT FILING DATE: 1998-02-18
; EARLIER APPLICATION NUMBER: 08/911,593

; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: 60/023,921
; EARLIER FILING DATE: 1996-08-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-025-596-34

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKK 4
|||
Db 3 AKKK 6

RESULT 3

US-09-579-664B-33

; Sequence 33, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-579-664B-33

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKKE 5
|||
Db 2 KKKE 5

RESULT 4

US-07-718-274A-31

; Sequence 31, Application US/07718274A
; Patent No. 5284756

; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/718,274A
; FILING DATE: 19910620
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/9430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-07-718-274A-31

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
|||
Db 5 KQR 7

RESULT 5
US-08-149-106-31

; Sequence 31, Application US/08149106
; Patent No. 5411941
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,106
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/9430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-149-106-31

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
|||
Db 5 KQR 7

RESULT 6
US-07-851-941-14
; Sequence 14, Application US/07851941
; Patent No. 5428016
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptide and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/851,941
; FILING DATE: 19920313
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/851,941
; FILING DATE: March 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:

; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:

US-07-851-941-14

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QRN 10
|||
Db 6 QRN 8

RESULT 7

US-07-694-983-15

; Sequence 15, Application US/07694983
; Patent No. 5432260
; GENERAL INFORMATION:
; APPLICANT: Stahl, Philip D.
; TITLE OF INVENTION: HIGH AFFINITY MANNOSE RECEPTOR
; TITLE OF INVENTION: LIGANDS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Irell & Manella
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/694,983

;
; FILING DATE: 19910503
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9500-0039.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /label= Ac-
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 11
; OTHER INFORMATION: /label= -NH2

US-07-694-983-15

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 2 KKK 4

RESULT 8

US-08-193-521-18

; Sequence 18, Application US/08193521
; Patent No. 5470950
; GENERAL INFORMATION:
; APPLICANT: Maloy, W. Lee
; APPLICANT: Kari, U. Prasad
; APPLICANT: Williams, Jon I.
; TITLE OF INVENTION: Biologically Active Peptide
; TITLE OF INVENTION: Compositions and Uses Therefor
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette

;
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,521
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,960
; FILING DATE:
; APPLICATION NUMBER: 07/760,054
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 421250-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide,
; OTHER INFORMATION: and/or may be acetylated at
; OTHER INFORMATION: N-terminus.

US-08-193-521-18

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 9

US-08-176-500-6

; Sequence 6, Application US/08176500
; Patent No. 5498538
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,500
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,416
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-08-176-500-6

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 10
US-08-298-021-31
; Sequence 31, Application US/08298021
; Patent No. 5508263
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Heterodimeric Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-64023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/298,021
;
; FILING DATE:
;
; CLASSIFICATION: 514
;
PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 08/149,106
;
; FILING DATE: 11-OCT-1993
;
PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 07/718,274
;
; FILING DATE: 20-JUN-1991
;
PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 07/415,555
;
; FILING DATE: 04-OCT-1989
;
PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 07/256,034
;
; FILING DATE: 11-OCT-1988
;
ATTORNEY/AGENT INFORMATION:
;
; NAME: Sharp, Jeffrey S.
;
; REGISTRATION NUMBER: 31,879
;
; REFERENCE/DOCKET NUMBER: 27129/32196
;
TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 312/474-6300
;
; TELEFAX: 312/474-0448
;
; TELEX: 25-3856
;
INFORMATION FOR SEQ ID NO: 31:
;
SEQUENCE CHARACTERISTICS:
;
; LENGTH: 11 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein

US-08-298-021-31

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
|||
Db 5 KQR 7

RESULT 11
US-08-116-733-32
;
; Sequence 32, Application US/08116733
;
; Patent No. 5516632
;
; GENERAL INFORMATION:
;
; APPLICANT: PALMER, Thomas J.
;
; APPLICANT: HAYNES, Barton F.
;
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
;
; NUMBER OF SEQUENCES: 46
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: NIXON & VANDERHYE P.C.
;
; STREET: 1100 NORTH GLEBE ROAD
;
; CITY: ARLINGTON

;
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-116-733-32

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
Db 2 AKK 4

RESULT 12
US-08-116-733-39
; Sequence 39, Application US/08116733
; Patent No. 5516632
; GENERAL INFORMATION:
; APPLICANT: PALKER, Thomas J.
; APPLICANT: HAYNES, Barton F.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-733-39

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RNA 11
 |||
Db 7 RNA 9

RESULT 13
US-08-178-570-75
; Sequence 75, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.

; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal

US-08-178-570-75

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 8 KKK 10

RESULT 14

US-08-471-052A-6

; Sequence 6, Application US/08471052A
; Patent No. 5625033
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 166
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,052A
; FILING DATE: 06-JUNE-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-471-052A-6

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
 |||
Db 1 EQK 3

RESULT 15

US-08-434-120-112

; Sequence 112, Application US/08434120
; Patent No. 5635479
; GENERAL INFORMATION:
; APPLICANT: Baker, Margaret A.
; APPLICANT: Jacob, Leonard S.
; APPLICANT: Maloy, W. Lee
; TITLE OF INVENTION: Treatment of Gynecological
; TITLE OF INVENTION: Malignancies with
; TITLE OF INVENTION: Biologically Active Peptides
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,120
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,950
; FILING DATE:
; APPLICATION NUMBER: US/08/226,108
; FILING DATE:
; APPLICATION NUMBER: US/07/937,462
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 421250-194

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-434-120-112

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AKK 3
Db 1 AKK 3

RESULT 16

US-08-465-325-111

; Sequence 111, Application US/08465325
; Patent No. 5686563
; GENERAL INFORMATION:
; APPLICANT: Magainin Pharmaceuticals Inc.
; APPLICANT: 5110 Campus Drive
; APPLICANT: Plymouth Meeting, PA 19462
; TITLE OF INVENTION: Biologically Active Peptides Having
; TITLE OF INVENTION: N-Terminal Substitutions
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,325
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,462
; FILING DATE: 18-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/891,201
; FILING DATE: 01-JUN-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B

; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0021-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-325-111

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 17

US-08-465-325-122

; Sequence 122, Application US/08465325
; Patent No. 5686563
; GENERAL INFORMATION:
; APPLICANT: Magainin Pharmaceuticals Inc.
; APPLICANT: 5110 Campus Drive
; APPLICANT: Plymouth Meeting, PA 19462
; TITLE OF INVENTION: Biologically Active Peptides Having
; TITLE OF INVENTION: N-Terminal Substitutions
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,325
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,462
; FILING DATE: 18-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/891,201
; FILING DATE: 01-JUN-92

; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0021-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-325-122

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 7 AKK 9

RESULT 18
US-08-465-325-123
; Sequence 123, Application US/08465325
; Patent No. 5686563
; GENERAL INFORMATION:
; APPLICANT: Magainin Pharmaceuticals Inc.
; APPLICANT: 5110 Campus Drive
; APPLICANT: Plymouth Meeting, PA 19462
; TITLE OF INVENTION: Biologically Active Peptides Having
; TITLE OF INVENTION: N-Terminal Substitutions
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,325
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,462
; FILING DATE: 18-JAN-94
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0021-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-465-325-123

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 7 AKK 9

RESULT 19

US-08-465-325-128

Sequence 128, Application US/08465325
Patent No. 5686563
GENERAL INFORMATION:
APPLICANT: Magainin Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: Plymouth Meeting, PA 19462
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I. Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462

;
; FILING DATE: 18-JAN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/891,201
; FILING DATE: 01-JUN-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0021-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-325-128

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 1 KKK 3

RESULT 20
US-08-416-035-8
; Sequence 8, Application US/08416035
; Patent No. 5739278
; GENERAL INFORMATION:
; APPLICANT: Daum, Gunter
; APPLICANT: Cool, Deborah E.
; APPLICANT: Fischer, Edmond H.
; TITLE OF INVENTION: Methods and Compositions for Protein
; TITLE OF INVENTION: Tyrosine Phosphatases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,035
; FILING DATE: 30-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: 08/059,949
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 940010.531
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-416-035-8

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 9 KKK 11

RESULT 21

US-08-189-331-6

;
; Sequence 6, Application US/08189331
; Patent No. 5747334
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/189,331
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

US-08-189-331-6

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
 |||
Db 1 EQK 3

RESULT 22

US-08-082-269D-2

; Sequence 2, Application US/08082269D
; Patent No. 5773227
; GENERAL INFORMATION:
; APPLICANT: Kuhn, Michael
; APPLICANT: Meyer, Tobias
; APPLICANT: Allbritton, Nancy
; TITLE OF INVENTION: Bifunctional Chelating Polysaccharides
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Molecular Probes, Inc.
; STREET: 4849 Pitchford Avenue
; CITY: Eugene
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97402-9144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS 6.2
; SOFTWARE: Text Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,269D
; FILING DATE: 23-June-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Helfenstein, Allegra J.
; REGISTRATION NUMBER: 34,179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503)465-8300
; TELEFAX: (503)344-6504
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 AMINO ACIDS
; TYPE: Amino Acid

;
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE:
; PUBLICATION INFORMATION:
; AUTHORS: Chelsky, Daniel, Ralph, Rebecca and Jonak, Gerald
; TITLE: Sequence Requirements for Synthetic Peptide-Mediated
Translocation to the
; Patent No. 5773227
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 9
; ISSUE: 6
; PAGES: 2487-2492
; DATE: 1989
US-08-082-269D-2

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 5 KKK 7

RESULT 23
US-07-803-623B-20
; Sequence 20, Application US/07803623B
; Patent No. 5773574
; GENERAL INFORMATION:
; APPLICANT: Ginsberg, Mark H
; APPLICANT: Plow, Edward F
; APPLICANT: Bowditch, Ronald
; TITLE OF INVENTION: NOVEL POLYPEPTIDES FOR PROMOTING CELL
; TITLE OF INVENTION: ATTACHMENT
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 5773574th Torrey Pines Road
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/803,623B
; FILING DATE: 27-NOV-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,668
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/725,600
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0601P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-07-803-623B-20

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RNA 11
|||
Db 7 RNA 9

RESULT 24
US-08-476-405A-14
Sequence 14, Application US/08476405A
Patent No. 5776459
GENERAL INFORMATION:
APPLICANT: Vandenbark, Arthur A.
TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connective Therapeutics, Inc.
STREET: 3400 West Bayshore Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,405A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,020
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: US 07/735,612
; FILING DATE: 16-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,022
; FILING DATE: 31-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/554,529
; FILING DATE: 19-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/467,577
; FILING DATE: 19-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/382,804
; FILING DATE: 19-JUL-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowin, David A.
; REGISTRATION NUMBER: 29,326
; REFERENCE/DOCKET NUMBER: 886 P15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-2800
; TELEFAX: 415-843-2899
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-476-405A-14

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QRN 10
|||
Db 7 QRN 9

RESULT 25

US-08-660-626-12

; Sequence 12, Application US/08660626
; Patent No. 5789655
; GENERAL INFORMATION:
; APPLICANT: Stanley B. Prusiner
; APPLICANT: Glenn C. Telling
; APPLICANT: Fred E. Cohen
; APPLICANT: Michael R. Scott
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
; TITLE OF INVENTION: EPITOPE-TAGGED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA

; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AscIII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,626
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Valeta Gregg
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 07532/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-660-626-12

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 26
US-08-478-386A-59
; Sequence 59, Application US/08478386A
; Patent No. 5830462
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,386A
; FILING DATE: 07/JUN/1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."
US-08-478-386A-59

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 27
US-08-292-597-59
; Sequence 59, Application US/08292597
; Patent No. 5834266
; GENERAL INFORMATION:
; APPLICANT: Gerald R. Crabtree
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: Regulated Apoptosis
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,597
; FILING DATE: 18/AUG/1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-108A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ
; OTHER INFORMATION: ID NOS:58 and 60."
US-08-292-597-59

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 28
US-08-967-101-183
; Sequence 183, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-101-183

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 29

US-08-806-084-20

; Sequence 20, Application US/08806084
; Patent No. 5843774
; GENERAL INFORMATION:
; APPLICANT: Ginsberg, Mark H
; APPLICANT: Plow, Edward F
; APPLICANT: Bowditch, Ronald
; TITLE OF INVENTION: NOVEL POLYPEPTIDES FOR PROMOTING CELL
; TITLE OF INVENTION: ATTACHMENT
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 5843774th Torrey Pines Road
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/806,084
FILING DATE: 25-FEB-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,623
FILING DATE: 27-NOV-1991
APPLICATION NUMBER: US 07/620,668
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/725,600
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0601P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

US-08-806-084-20

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RNA 11
 |||
Db 7 RNA 9

RESULT 30

US-08-471-939-6

Sequence 6, Application US/08471939
Patent No. 5844076
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,939
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/013,416
; FILING DATE: 01-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-939-6

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 31
US-08-701-124-19
; Sequence 19, Application US/08701124
; Patent No. 5846782
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-701-124-19

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 3 KKK 5

RESULT 32
US-08-621-803-206
; Sequence 206, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 206:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.350"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-206

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 1 KKK 3

RESULT 33

US-08-471-800-6

; Sequence 6, Application US/08471800
; Patent No. 5852167
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,800
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/013,416
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-143
; TELECOMMUNICATION INFORMATION:

;
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-800-6

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
 |||
Db 1 EQK 3

RESULT 34

US-08-621-259A-181

;
; Sequence 181, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G
; APPLICANT: Lim, Edward
; APPLICANT: Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,259A
; FILING DATE: 21-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/504,841
; FILING DATE: 20-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11021US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX:

; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "XMP.350"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: C-Terminus
; OTHER INFORMATION: /label= Amidation
; OTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-259A-181

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 1 KKK 3

RESULT 35
US-08-002-324-5
; Sequence 5, Application US/08002324
; Patent No. 5861156
; GENERAL INFORMATION:
; APPLICANT: George, Andrew J.T.
; APPLICANT: Segal, David M.
; APPLICANT: Huston, James S.
; TITLE OF INVENTION: METHODS OF DELIVERING AGENTS TO TARGET
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,324
; FILING DATE: 19930108
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CBM92-02
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 981-6240
; TELEFAX: (617) 981-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-002-324-5

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 36

US-08-388-653-59

; Sequence 59, Application US/08388653

; Patent No. 5869337

; GENERAL INFORMATION:

; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter

; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/388,653
; FILING DATE: 14-FEB-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,386
; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195

; REFERENCE/DOCKET NUMBER: 2054-114A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 783-6040

; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."
US-08-388-653-59

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 4 KKK 6

RESULT 37
US-08-473-985-59
; Sequence 59, Application US/08473985
; Patent No. 5871753
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; APPLICANT: Ho, Steffan
; TITLE OF INVENTION: Regulated Transcription of Targeted Genes and
; TITLE OF INVENTION: Other Biological Events
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,748
; FILING DATE: 07-JAN-1994
; ATTORNEY/AGENT INFORMATION:

;
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-SU 9863
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ
; OTHER INFORMATION: ID NOS:58 and 60."
US-08-473-985-59

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 38
US-08-538-960-8

; Sequence 8, Application US/08538960
; Patent No. 5872230
; GENERAL INFORMATION:
; APPLICANT: Stocco, Douglas M.
; APPLICANT: Clark, Barbara J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: REGULATION OF STEROIDOGENESIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
; STREET: 1900 Frost Bank Plaza, 816 Congress Avenue
; CITY: Austin
; STATE: TX
; COUNTRY: U.S.A.
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,960
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732

; REFERENCE/DOCKET NUMBER: 43375.0002/DLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/499-6200
; TELEFAX: 512/499-6290
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-538-960-8

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
|||
Db 9 KKE 11

RESULT 39
US-08-760-075A-1
; Sequence 1, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-075A-1

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
|||
Db 9 KKE 11

RESULT 40

US-08-471-068-6

; Sequence 6, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-6

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 41
US-08-475-081-1

; Sequence 1, Application US/08475081
; Patent No. 5948894
; GENERAL INFORMATION:
; APPLICANT: Berry, Mark J.
; APPLICANT: Davis, Paul J.
; APPLICANT: Verhoeven, Martine E.
; APPLICANT: De Winter, Ronald F.J.
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,081
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/979,448
; FILING DATE: 20-NOV-1992
; APPLICATION NUMBER: US/07/628,910
; FILING DATE: 18-DEC-1990
; APPLICATION NUMBER: GB 8928501.9
; FILING DATE: 18-DEC-1990
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 248453 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
US-08-475-081-1

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 42

US-08-564-063-26

; Sequence 26, Application US/08564063

; Patent No. 5962418

; GENERAL INFORMATION:

; APPLICANT: SAKARIASSEN, Kjell S

; APPLICANT: STEPHENS, Ross W

; APPLICANT: ORNING, Lars

; TITLE OF INVENTION: FACTOR VII-DERIVED PEPTIDES

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Testa, Hurwitz & Thibeault, LLP

; STREET: 125 High Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/564,063

; FILING DATE: 28-MAY-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: CAMPBELL, Paula A

; REGISTRATION NUMBER: 32,503

; REFERENCE/DOCKET NUMBER: FRD-006

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-564-063-26

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RNA 11
|||
Db 9 RNA 11

RESULT 43

US-08-592-541-183

; Sequence 183, Application US/08592541

; Patent No. 5986054

; GENERAL INFORMATION:

; APPLICANT: ST. GEORGE-HYSLOP, PETER H

; APPLICANT: ROMMENS, JOHANNA M

; APPLICANT: FRASER, PAUL E

; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

; NUMBER OF SEQUENCES: 183

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TESTA, HURWITZ & THIBEAULT

; STREET: High Street Tower - 125 High Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/592,541

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Pitcher, Edmund R.

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 183:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-592-541-183

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 44
US-08-538-711A-3
; Sequence 3, Application US/08538711A
; Patent No. 5994062
; GENERAL INFORMATION:
; APPLICANT: MULSHINE, JAMES, L.
; TITLE OF INVENTION: AN EPITHELIAL PROTEIN AND
; TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,711A
; FILING DATE: 02-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KATHRYN M. BROWN
; REGISTRATION NUMBER: 34,556
; REFERENCE/DOCKET NUMBER: 2026-4201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-08-538-711A-3

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEQ 6
|||
Db 3 KEQ 5

RESULT 45
US-08-483-898-59
; Sequence 59, Application US/08483898
; Patent No. 5994313

; GENERAL INFORMATION:
; APPLICANT: Gerald R. Crabtree
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: Regulated Apoptosis
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,898
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,597
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-108A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ
; OTHER INFORMATION: ID NOS:58 and 60."
US-08-483-898-59

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 4 KKK 6

US-08-105-904B-9

; Sequence 9, Application US/08105904B

; Patent No. 6001364

; GENERAL INFORMATION:

; APPLICANT: Rose, Keith

; APPLICANT: Offord, Robin

; TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR

; TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

; STREET: 5 Palo Alto Square, 3000 El Camino Real

; CITY: Palo Alto

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/105,904B

; FILING DATE: 31-AUG-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/057,594

; FILING DATE: 05-MAY-1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Neeley, Richard L.

; REGISTRATION NUMBER: 30,092

; REFERENCE/DOCKET NUMBER: ABIC-001/02US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)843-5000

; TELEFAX: (415)857-0663

; TELEX: 380816 CooleyPA

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; OTHER INFORMATION: GXL-Gly

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 4

; OTHER INFORMATION: Lys-GXL

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 5

; OTHER INFORMATION: Lys-GXL

; FEATURE:

; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: Lys-GXL
FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: Lys-GXL
FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: Lys-GXL
FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: Lys-GXL
FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: Lys-GXL
US-08-105-904B-9

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 47

US-08-105-904B-21
; Sequence 21, Application US/08105904B
; Patent No. 6001364
; GENERAL INFORMATION:
; APPLICANT: Rose, Keith
; APPLICANT: Offord, Robin
; TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR
; TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,904B
; FILING DATE: 31-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

;
; APPLICATION NUMBER: US 08/057,594
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: ABIC-001/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5000
; TELEFAX: (415) 857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: Gly-PAM

US-08-105-904B-21

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4

Db |||
 4 KKK 6

RESULT 48
US-08-369-643-75
; Sequence 75, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; OTHER INFORMATION: synthesized as a substrate for cyclin containing
; OTHER INFORMATION: kinases
US-08-369-643-75

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 8 KKK 10

RESULT 49
US-09-087-716-59
; Sequence 59, Application US/09087716
; Patent No. 6011018
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA

; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,716
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,653
; FILING DATE: 02/14/1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."
US-09-087-716-59

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 50

US-09-139-762A-124

; Sequence 124, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington

;
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-139-762A-124

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 51
US-08-518-835-4
; Sequence 4, Application US/08518835
; Patent No. 6017754
; GENERAL INFORMATION:
; APPLICANT: CHESTNUT, JONATHAN D.
; APPLICANT: HOEFFLER, JAMES P.
; TITLE OF INVENTION: NOVEL SYSTEM FOR ISOLATING AND
; TITLE OF INVENTION: IDENTIFYING EUKARYOTIC CELLS TRANSFECTED WITH GENES
AND
; TITLE OF INVENTION: VECTORS, HOST CELLS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,835
; FILING DATE: 24-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGIGLIO, FRANK S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 11093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-518-835-4

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 52

US-08-970-833-8

; Sequence 8, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Kiessling, Laura L.
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-970-833-8

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 6 KKK 8

RESULT 53
US-08-836-337-3
; Sequence 3, Application US/08836337
; Patent No. 6025544
; GENERAL INFORMATION:
; APPLICANT: Leggewie, Georg
; APPLICANT: Riesmeier, Jorg
; APPLICANT: Frommer, Wolf-Bernd
; TITLE OF INVENTION: PROCESSES FOR MODIFYING PLANT FLOWERING
; TITLE OF INVENTION: BEHAVIOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,337

; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 39 748.8
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: AGREVO-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-337-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 54
US-09-015-003-5
; Sequence 5, Application US/09015003
; Patent No. 6030783
; GENERAL INFORMATION:
; APPLICANT: KANE, Stefanie A.
; APPLICANT: LIPPARD, Stephen J.
; TITLE OF INVENTION: Photo-Potentiation of Cisplatin
; TITLE OF INVENTION: Chemotherapy
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator, Testa, Hurwitz &
; ADDRESSEE: Thibeault, LLP
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,003
; FILING DATE:
; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON, Gillian M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: MIT-079
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-09-015-003-5

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 2 KKK 4

RESULT 55

US-08-159-339A-1148

; Sequence 1148, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746

;
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1148

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QKQ 8
|||
Db 6 QKQ 8

RESULT 56

US-09-157-753-59

;
; Sequence 59, Application US/09157753
; Patent No. 6043082
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,753
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,653
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: US 08/478,386
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."
US-09-157-753-59

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 57
US-09-157-230-59
; Sequence 59, Application US/09157230
; Patent No. 6046047
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,230
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,386
; FILING DATE: 07/JUN/1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."
US-09-157-230-59

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 58
US-09-087-811-59
; Sequence 59, Application US/09087811
; Patent No. 6054436
; GENERAL INFORMATION:
; APPLICANT: Gerald R. Crabtree
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: Regulated Apoptosis
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA

; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,811
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,597
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-108A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ
; OTHER INFORMATION: ID NOS:58 and 60."
US-09-087-811-59

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 59
US-09-130-225-19
; Sequence 19, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago

;
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,225
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-130-225-19

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 3 KKK 5

RESULT 60
US-08-968-747-8
; Sequence 8, Application US/08968747
; Patent No. 6060595
; GENERAL INFORMATION:
; APPLICANT: Scaglioni et al.
; TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,747
; FILING DATE: 03-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.

; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08472/705001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-968-747-8

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 61

US-09-156-855-59

; Sequence 59, Application US/09156855
; Patent No. 6063625
; GENERAL INFORMATION:
; APPLICANT: Gerald R. Crabtree
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: Regulated Transcription of Targeted
; TITLE OF INVENTION: Genes and Other Biological Events
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/156,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/196,043
; FILING DATE: 11-FEB-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: Berstein, David L.
; REGISTRATION NUMBER: 31,235
; REFERENCE/DOCKET NUMBER: ARIAD 316C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0400
; TELEFAX: (617) 494-8144
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ
; OTHER INFORMATION: ID NOS:58 and 60."
US-09-156-855-59

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 62

US-09-188-579-65

; Sequence 65, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 65
; LENGTH: 11
; TYPE: PRT
; ORGANISM: vaccinia virus
; FEATURE:
; OTHER INFORMATION: Motif V of RNA guanylyltransferase.
US-09-188-579-65

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
 |||
Db 5 KKE 7

RESULT 63

US-09-212-971-17
; Sequence 17, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Based on Homo sapiens sequence

US-09-212-971-17

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 64

US-08-971-692-37

; Sequence 37, Application US/08971692
; Patent No. 6114147
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Immobilized proteins with specific binding
; TITLE OF INVENTION: capacities and their use in processes and products.
; NUMBER OF SEQUENCES: 40
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,692

;
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Myc tail
US-08-971-692-37

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 65

US-09-124-698-183

; Sequence 183, Application US/09124698
; Patent No. 6117978
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,698
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100

; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-124-698-183

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 66

US-08-893-749-17

; Sequence 17, Application US/08893749
; Patent No. 6126916
; GENERAL INFORMATION:
; APPLICANT: MCBRIDE, William J.
; APPLICANT: GRIFFITHS, Gary L.
; TITLE OF INVENTION: RADIOMETAL-BINDING PEPTIDE ANALOGUES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,749
; FILING DATE: 11-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,662
; FILING DATE: 12-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bern D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 018733/0804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

;
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "Xaa is D-Phe"
;
FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Xaa is D-Trp"
US-08-893-749-17

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 1 KKK 3

RESULT 67
US-08-493-071-22
;
Sequence 22, Application US/08493071

;
Patent No. 6127149
;
GENERAL INFORMATION:
;
APPLICANT: Hirai, Yohei
;
APPLICANT: Koshida, Shogo
;
APPLICANT: Oka, Yumiko
;
TITLE OF INVENTION: MODIFIED EPIMORPHIN
;
NUMBER OF SEQUENCES: 30
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
;
STREET: 99 CANAL CENTER PLAZA, SUITE 300
;
CITY: ALEXANDRIA
;
STATE: VA
;
COUNTRY: USA
;
ZIP: 22314
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Floppy disk
;
COMPUTER: IBM PC compatible
;
OPERATING SYSTEM: PC-DOS/MS-DOS
;
SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/08/493,071
;
FILING DATE:
;
CLASSIFICATION: 435
;
ATTORNEY/AGENT INFORMATION:
;
NAME: Price, Robert L.
;
REGISTRATION NUMBER: 22,685
;
REFERENCE/DOCKET NUMBER: 715-107
;
TELECOMMUNICATION INFORMATION:
;
TELEPHONE: 703-684-1111
;
TELEFAX: 703-684-1124
;
INFORMATION FOR SEQ ID NO: 22:
;
SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-493-071-22

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 68
US-08-800-929A-17
; Sequence 17, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF
PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-800-929A-17

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 69
US-09-158-010-59
; Sequence 59, Application US/09158010
; Patent No. 6140120
; GENERAL INFORMATION:
; APPLICANT: Gerald R. Crabtree
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: Regulated Transcription of Targeted
; TITLE OF INVENTION: Genes and Other Biological Events
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,010
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/196,043
; FILING DATE: 11-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernstein, David L.
; REGISTRATION NUMBER: 31,235

; REFERENCE/DOCKET NUMBER: ARIAD 316C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 494-0400
; TELEFAX: (617) 494-8144
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ
; OTHER INFORMATION: ID NOS:58 and 60."
US-09-158-010-59

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 70
US-09-031-168-12
; Sequence 12, Application US/09031168
; Patent No. 6150583
; GENERAL INFORMATION:
; APPLICANT: Stanley B. Prusiner
; APPLICANT: Glenn C. Telling
; APPLICANT: Fred E. Cohen
; APPLICANT: Michael R. Scott
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
; TITLE OF INVENTION: EPITOPE-TAGGED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,168
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/660,626
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: Valeta Gregg
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 07532/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-031-168-12

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
 |||
Db 1 EQK 3

RESULT 71
US-08-861-745B-5
; Sequence 5, Application US/08861745B
; Patent No. 6165733
; GENERAL INFORMATION:
; APPLICANT: Cen, Hui
; APPLICANT: Williams, Lewis
; TITLE OF INVENTION: Gamma II Adapton
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,745B
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 02441.05336

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6165733e
US-08-861-745B-5

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 72

US-08-341-560B-23

; Sequence 23, Application US/08341560B
; Patent No. 6165745
; GENERAL INFORMATION:
; APPLICANT: Ward, E. Sally
; APPLICANT: Kim, Jin-Kyoo
; TITLE OF INVENTION: Recombinant Production of
; TITLE OF INVENTION: Immunoglobulin-Like Domains in Prokaryotic Cells
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 7721-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/341,560B
; FILING DATE: 17-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,333
; FILING DATE: 19-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/873,930
; FILING DATE: 24-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165

; REFERENCE/DOCKET NUMBER: UTSD:353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-341-560B-23

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 73

US-09-087-647-59

; Sequence 59, Application US/09087647

; Patent No. 6165787

; GENERAL INFORMATION:

; APPLICANT: Crabtree, Gerald R.

; APPLICANT: Schreiber, Stuart L.

; APPLICANT: Spencer, David M.

; APPLICANT: Wandless, Thomas J.

; APPLICANT: Belshaw, Peter

; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED

; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS

; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARIAD Pharmaceuticals, Inc.

; STREET: 26 Lansdowne Street

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02139

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC/DOS/MS/DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/087,647

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,386

; FILING DATE: 07/JUN/1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Figg, E. Anthony

; REGISTRATION NUMBER: 27,195

; REFERENCE/DOCKET NUMBER: 2054-114A

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Translation product of SEQ ID
; OTHER INFORMATION: NOS:58 and 60."
US-09-087-647-59

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 74
US-08-114-877A-9
; Sequence 9, Application US/08114877A
; Patent No. 6174530
; GENERAL INFORMATION:
; APPLICANT: Rose, Keith
; APPLICANT: Offord, Robin
; TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
; TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,877A
; FILING DATE: 31-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,594
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.

;
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: ABIC-001/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843 5070
; TELEFAX: (415) 857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: GLX-Gly
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: Lys-GLX
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: Lys-GLX
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: Lys-GLX
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: Lys-GLX
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: Lys-GLX
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: Lys-GLX
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: Lys-GLX
US-08-114-877A-9

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

RESULT 75

US-08-114-877A-14
; Sequence 14, Application US/08114877A
; Patent No. 6174530
; GENERAL INFORMATION:
; APPLICANT: Rose, Keith
; APPLICANT: Offord, Robin
; TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
; TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,877A
; FILING DATE: 31-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,594
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: ABIC-001/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843 5070
; TELEFAX: (415) 857-0663
; TELEX: 380816 CooleyPA
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: Lys-BOC
; FEATURE:

;
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: Lys-BOC
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: Gly-PAM
US-08-114-877A-14

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 4 KKK 6

Search completed: April 8, 2004, 15:52:15
Job time : 12.3077 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds
(without alignments)
122.816 Million cell updates/sec

Title: US-09-787-443A-20

Perfect score: 11

Sequence: 1 AKKKEQKQRNA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	3	27.3	11	2	PD0441	translation elonga
2	2	18.2	11	1	GMROL	leucosulfakinin -
3	2	18.2	11	2	G42762	proteasome endopep
4	2	18.2	11	2	A33917	dihydroorotate (EC
5	2	18.2	11	2	A38841	rhodopsin homolog
6	2	18.2	11	2	PQ0682	photosystem I 17.5
7	2	18.2	11	2	C53652	rhlR protein - Pse
8	2	18.2	11	2	S07203	uperolein - frog (
9	2	18.2	11	2	S42449	ant1 protein - pha
10	2	18.2	11	2	JQ0395	hypothetical prote
11	2	18.2	11	2	PQ0231	beta-glucosidase (
12	2	18.2	11	2	S66606	quinoline 2-oxidor
13	2	18.2	11	2	S42587	celF protein - Esc

14	2	18.2	11	2	S33782	acetolactate synth
15	2	18.2	11	2	B43669	hypothetical prote
16	2	18.2	11	2	PC2372	58K heat shock pro
17	2	18.2	11	2	B41835	translation elonga
18	2	18.2	11	2	S33519	probable secreted
19	2	18.2	11	2	PT0081	protein QA300023 -
20	2	18.2	11	2	PA0028	protein QA300042 -
21	2	18.2	11	2	G61497	seed protein ws-23
22	2	18.2	11	2	S19775	wound-induced prot
23	2	18.2	11	2	PU0029	33K protein 3218 -
24	2	18.2	11	2	PN0167	ribosomal protein
25	2	18.2	11	2	A26120	6-phosphofructokin
26	2	18.2	11	2	A60656	perisulfakinin - A
27	2	18.2	11	2	S68637	acetylcholinester
28	2	18.2	11	2	A33571	follistatin - bovi
29	2	18.2	11	2	S54347	tubulin beta chain
30	2	18.2	11	2	A14454	6-phosphofructokin
31	2	18.2	11	2	A61483	pyridoxal kinase (
32	2	18.2	11	2	PH1376	T antigen variant
33	2	18.2	11	2	PT0214	T-cell receptor be
34	2	18.2	11	2	S53436	beta-D-galactosida
35	2	18.2	11	2	S65377	cytochrome-c oxida
36	2	18.2	11	2	PH0941	T-cell receptor be
37	2	18.2	11	2	PH0929	T-cell receptor be
38	2	18.2	11	2	PH0924	T-cell receptor be
39	2	18.2	11	2	PH0919	T-cell receptor be
40	2	18.2	11	2	PH0914	T-cell receptor be
41	2	18.2	11	2	H84082	hypothetical prote
42	2	18.2	11	4	S19015	hypothetical prote
43	1	9.1	11	1	XAVIBH	bradykinin-potenti
44	1	9.1	11	1	XASNBA	bradykinin-potenti
45	1	9.1	11	1	ECLQ2M	tachykinin II - mi
46	1	9.1	11	1	SPHO	substance P - hors
47	1	9.1	11	1	EOOCC	eledoisin - curled
48	1	9.1	11	1	A60654	substance P - guin
49	1	9.1	11	1	EOOC	eledoisin - musky
50	1	9.1	11	1	LFTWWE	probable trpEG lea
51	1	9.1	11	2	S66196	alcohol dehydrogen
52	1	9.1	11	2	S68392	H+-transporting tw
53	1	9.1	11	2	B49164	chromogranin-B - r
54	1	9.1	11	2	JN0023	substance P - chic
55	1	9.1	11	2	S32575	ribosomal protein
56	1	9.1	11	2	A40693	transgelin - sheep
57	1	9.1	11	2	S00616	parasporal crystal
58	1	9.1	11	2	A57458	gene Gax protein -
59	1	9.1	11	2	A26930	ermG leader peptid
60	1	9.1	11	2	D60409	kassinin-like pept
61	1	9.1	11	2	F60409	substance P-like p
62	1	9.1	11	2	E60409	substance P-like p
63	1	9.1	11	2	YHRT	morphogenetic neur
64	1	9.1	11	2	YHHU	morphogenetic neur
65	1	9.1	11	2	YHBO	morphogenetic neur
66	1	9.1	11	2	YHXAE	morphogenetic neur
67	1	9.1	11	2	YHJFHY	morphogenetic neur
68	1	9.1	11	2	A61365	phyllokinin - Rohd
69	1	9.1	11	2	B26744	megascoliakinin -
70	1	9.1	11	2	S23308	substance P - rain

71	1	9.1	11	2	S23306	substance P - Atla
72	1	9.1	11	2	B60409	kassinin-like pept
73	1	9.1	11	2	C60409	kassinin-like pept
74	1	9.1	11	2	S07207	Crinia-angiotensin
75	1	9.1	11	2	S07201	physalaemin - frog
76	1	9.1	11	2	A61033	ranatachakinin A -
77	1	9.1	11	2	D61033	ranatachakinin D -
78	1	9.1	11	2	B58501	24K kidney and bla
79	1	9.1	11	2	D58502	27K bile and gallb
80	1	9.1	11	2	A58502	38K kidney stone p
81	1	9.1	11	2	C58501	42K bile stone pro
82	1	9.1	11	2	F58501	43.5K bile stone p
83	1	9.1	11	2	S58244	pyrroloquinoline q
84	1	9.1	11	2	S04875	nifS protein - Bra
85	1	9.1	11	2	I41138	acetyl ornithine d
86	1	9.1	11	2	S35490	type II site-speci
87	1	9.1	11	2	S21127	precorrin methyltr
88	1	9.1	11	2	S70720	trigger factor hom
89	1	9.1	11	2	B39853	LuxC protein - Pho
90	1	9.1	11	2	A58838	hemolysin - Porphy
91	1	9.1	11	2	E60691	phycobilisome 8K l
92	1	9.1	11	2	D60691	phycobilisome 9K l
93	1	9.1	11	2	PC2330	cycloinulooligosac
94	1	9.1	11	2	S14087	parasporal crystal
95	1	9.1	11	2	A44755	20alpha-hydroxyste
96	1	9.1	11	2	E41476	probable antigen 5
97	1	9.1	11	2	A55149	tetracenomycin A2
98	1	9.1	11	2	S19301	endo-1,4-beta-xyla
99	1	9.1	11	2	H54346	pyruvate synthase
100	1	9.1	11	2	S70338	napin small chain

ALIGNMENTS

RESULT 1

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse
(fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||
Db 4 AKK 6

RESULT 2

GMROL

leucosulfakinin - Madeira cockroach

N;Alternate names: LSK

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996

C;Accession: A01622

R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.

A;Reference number: A01622; MUID:86315858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; hormone; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6

||

Db 1 EQ 2

RESULT 3

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003

C;Accession: G42762

R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
Biochemistry 31, 7347-7355, 1992

A;Title: Identification and localization of a cysteinyl residue critical for the trypsin-like catalytic activity of the proteasome.

A;Reference number: A42762; MUID:92378961; PMID:1510924

A;Accession: G42762

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DIC>

A;Note: sequence extracted from NCBI backbone (NCBIP:112176)

C;Superfamily: multicatalytic endopeptidase complex chain C9

C;Keywords: hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QK 7

Db ||
7 QK 8

RESULT 4

A33917

dihydroorotate (EC 3.5.2.3) - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997

C;Accession: A33917

R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.;
Bergh, S.T.; Evans, D.R.

Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989

A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase
domain and interdomain linker in the CAD multifunctional polypeptide and
properties of the isolated domain.

A;Reference number: A33917; MUID:89282776; PMID:2543974

A;Accession: A33917

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <SIM>

A;Cross-references: GB:M23652

C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase
homology; Bacillus dihydroorotate homology; biotin carboxylase homology;
carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase
(glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase
(glutamine-hydrolyzing) small chain homology; trpG homology

C;Keywords: hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QK 7
 ||
Db 4 QK 5

RESULT 5

A38841

rhodopsin homolog - squid (Watasenia scintillans) (fragment)

N;Alternate names: visual pigment protein

C;Species: Watasenia scintillans (sparkling enope)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Oct-1997

C;Accession: A38841

R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.

Biochim. Biophys. Acta 957, 318-321, 1988

A;Title: Amino acid sequence of the retinal binding site of squid visual
pigment.

A;Reference number: PT0063; MUID:89051045; PMID:3191148

A;Accession: A38841

A;Molecule type: protein

A;Residues: 1-11 <SEI>

C;Superfamily: vertebrate rhodopsin

C;Keywords: chromoprotein; retinal

F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 2 AK 3

RESULT 6

PQ0682

photosystem I 17.5K D2 chain - common tobacco (fragment)

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

C;Accession: PQ0682

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are all present in isoforms in Nicotiana spp.

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0682

A;Molecule type: protein

A;Residues: 1-11 <OBO>

C;Superfamily: photosystem I chain II

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 7 KE 8

RESULT 7

C53652

rhlR protein - Pseudomonas aeruginosa (fragment)

C;Species: Pseudomonas aeruginosa

C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Aug-1998

C;Accession: C53652

R;Ochsner, U.A.; Fiechter, A.; Reiser, J.

J. Biol. Chem. 269, 19787-19795, 1994

A;Title: Isolation, characterization, and expression in Escherichia coli of the Pseudomonas aeruginosa rhlAB genes encoding a rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis.

A;Reference number: A53652; MUID:94327521; PMID:8051059

A;Accession: C53652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <OCH>

A;Cross-references: GB:L28170

C;Superfamily: sdiA regulatory protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10
||
Db 2 RN 3

RESULT 8
S07203
uperolein - frog (Uperoleia marmorata)
C;Species: Uperoleia marmorata
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07203
R;Anastasi, A.; Erspamer, V.; Endean, R.
Experientia 31, 394-395, 1975
A;Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in
the skin of Uperoleia rugosa and Uperoleia marmorata.
A;Reference number: S07203; MUID:75131227; PMID:1120493
A;Accession: S07203
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 5 NA 6

RESULT 9
S42449
antI protein - phage P7
C;Species: phage P7
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C;Accession: S42449
R;Citron, M.; Schuster, H.
Cell 62, 591-598, 1990
A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A;Reference number: S42448; MUID:90335968; PMID:1696181
A;Accession: S42449
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-11 <CIT>
A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 2 KK 3

RESULT 10

JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans

N;Alternate names: hypothetical 1.4K protein

C;Species: Azorhizobium caulinodans

A;Note: host Sesbania rostrata

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Feb-1994

C;Accession: JQ0395

R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.

Mol. Genet. 219, 289-298, 1989

A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans: nucleotide sequence and plant-inducible expression.

A;Reference number: JQ0393; MUID:90136519; PMID:2615763

A;Accession: JQ0395

A;Molecule type: DNA

A;Residues: 1-11 <GOE>

A;Cross-references: GB:L18897

A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3

||

Db 6 KK 7

RESULT 11

PQ0231

beta-glucosidase (EC 3.2.1.21) - Cellvibrio gilvus (fragment)

C;Species: Cellvibrio gilvus

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 07-May-1999

C;Accession: PQ0231

R;Kashiwagi, Y.; Iijima, C.; Sasaki, T.; Taniguchi, H.

Agric. Biol. Chem. 55, 2553-2559, 1991

A;Title: Characterization of a beta-glucosidase encoded by a gene from Cellvibrio gilvus.

A;Reference number: PQ0231; MUID:92144103; PMID:1368758

A;Accession: PQ0231

A;Molecule type: protein

A;Residues: 1-11 <KAS>

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QK 7

||

Db 9 QK 10

RESULT 12

S66606

quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)
C;Species: Comamonas testosteroni
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S66606
R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.
Eur. J. Biochem. 232, 536-544, 1995
A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.
A;Reference number: S66606; MUID:96035889; PMID:7556204
A;Accession: S66606
A;Molecule type: protein
A;Residues: 1-11 <SCH>
A;Experimental source: strain 63

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 13
S42587
celF protein - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S42587
R;Guzzo, A.; DuBow, M.S.
Mol. Gen. Genet. 242, 455-460, 1994
A;Title: A luxAB transcriptional fusion to the cryptic celF gene of Escherichia coli displays increased luminescence in the presence of nickel.
A;Reference number: S42587; MUID:94166755; PMID:8121401
A;Accession: S42587
A;Molecule type: DNA
A;Residues: 1-11 <GUZ>
C;Genetics:
A;Gene: celF

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10
||
Db 2 RN 3

RESULT 14
S33782
acetolactate synthase (EC 4.1.3.18) small chain, valine-sensitive - Serratia marcescens (fragment)
C;Species: Serratia marcescens
C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: S33782

R;Yang, J.H.; Kim, S.S.
Biochim. Biophys. Acta 1157, 178-184, 1993
A;Title: Purification and characterization of the valine sensitive acetolactate synthase from *Serratia marcescens* ATCC 25419.
A;Reference number: S33781; MUID:93283409; PMID:8507653
A;Accession: S33782
A;Molecule type: protein
A;Residues: 1-11 <YAN>
A;Experimental source: ATCC 25419
C;Complex: heterotetramer; two small and two large chains
C;Function:
A;Description: catalyzes the condensation of pyruvate and alpha-ketobutyrate to form alpha-aceto-alpha-hydroxybutyrate
A;Pathway: valine, leucine, and isoleucine biosynthesis
A;Note: this isoenzyme exhibits homotropic allosterism with pyruvate
C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; heterotetramer; magnesium; oxo-acid-lyase; valine inhibition

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10
||
Db 6 RN 7

RESULT 15
B43669
hypothetical protein (rhdA 5' region) - *Synechococcus* sp. (fragment)
C;Species: *Synechococcus* sp.
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C;Accession: B43669
R;Laudenbach, D.E.; Ehrhardt, D.; Green, L.; Grossman, A.
J. Bacteriol. 173, 2751-2760, 1991
A;Title: Isolation and characterization of a sulfur-regulated gene encoding a periplasmically localized protein with sequence similarity to rhodanese.
A;Reference number: A43669; MUID:91210163; PMID:1708376
A;Accession: B43669
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <LAU>
A;Cross-references: GB:M65244

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 6 AK 7

RESULT 16
PC2372
58K heat shock protein groEL [similarity] - *Bacillus cereus* (strain ts-4)
(fragment)

C;Species: *Bacillus cereus*
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PC2372
R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A;Title: Identification of DNA-binding proteins changed after induction of sporulation in *Bacillus cereus*.
A;Reference number: PC2369; MUID:95218265; PMID:7766022
A;Accession: PC2372
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <MAS>
C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 17
B41835
translation elongation factor EF-G homolog - *Bacillus subtilis* (fragment)
C;Species: *Bacillus subtilis*
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Dec-1997
C;Accession: B41835
R;Mitchell, C.; Morris, P.W.; Vary, J.C.
J. Bacteriol. 174, 2474-2477, 1992
A;Title: Identification of proteins phosphorylated by ATP during sporulation of *Bacillus subtilis*.
A;Reference number: A41835; MUID:92210489; PMID:1556067
A;Accession: B41835
A;Molecule type: protein
A;Residues: 1-11 <MIT>
A;Note: this protein is phosphorylated during stationary phase but not during exponential growth
C;Keywords: phosphoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10
||
Db 7 RN 8

RESULT 18
S33519
probable secreted protein - *Acholeplasma laidlawii* (fragment)
C;Species: *Acholeplasma laidlawii*
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999
C;Accession: S33519

R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.
submitted to the EMBL Data Library, June 1993
A;Description: Sequence regions from Acholeplasma laidlawii which restore export
of beta-lactamase in Escherichia coli.
A;Reference number: S33518
A;Accession: S33519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <BOY>
A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 2 KK 3

RESULT 19
PT0081
protein QA300023 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 24-Nov-1999
C;Accession: PT0081
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and
standardization of the gel patterns.
A;Reference number: PN0173
A;Accession: PT0081
A;Molecule type: protein
A;Residues: 1-11 <TSU>
A;Experimental source: Leaf
C;Keywords: acetylated amino end
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 2 KE 3

RESULT 20
PA0028
protein QA300042 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0028
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-
dimensional gel electrophoresis.

A;Reference number: PA0001
A;Accession: PA0028
A;Molecule type: protein
A;Residues: 1-11 <KAM>
A;Experimental source: seed
C;Keywords: seed

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 10 NA 11

RESULT 21

G61497
seed protein ws-23 - winged bean (fragment)
C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: G61497
R;Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-dimensional gel.
A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: G61497
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <HIR>
C;Keywords: glycoprotein; seed

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 22

S19775
wound-induced protein - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
C;Accession: S19775
R;Parsons, B.L.
submitted to the EMBL Data Library, May 1991
A;Reference number: S19773
A;Accession: S19775
A;Molecule type: mRNA
A;Residues: 1-11 <PAR>
A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 5 KK 6

RESULT 23

PU0029

33K protein 3218 - rice (strain Nohonbare) (fragment)

C;Species: Oryza sativa (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C;Accession: PU0029

R;Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993

A;Reference number: PS0208

A;Accession: PU0029

A;Molecule type: protein

A;Residues: 1-11 <TSU>

A;Experimental source: bran

C;Comment: molecular weight 33K, pI 6.0.

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||
Db 10 EQ 11

RESULT 24

PN0167

ribosomal protein S12 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 05-Aug-1994

C;Accession: PN0167

R;Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium
sporotrichioides proteins and the partial amino acid sequence of a peptidyl-
prolyl cis-trans isomerase.

A;Reference number: PN0160

A;Accession: PN0167

A;Molecule type: protein

A;Residues: 1-11 <FUK>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 4 KQ 5

RESULT 25

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)

N;Alternate names: phosphofructokinase; phosphohexokinase

C;Species: Ascaris suum (pig roundworm)

C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 28-Apr-1993

C;Accession: A26120

R;Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.

J. Biol. Chem. 262, 32-34, 1987

A;Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequence of the phosphopeptide.

A;Reference number: A26120; MUID:87083467; PMID:3025208

A;Accession: A26120

A;Molecule type: protein

A;Residues: 1-11 <KUL>

C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 26

A60656

perisulfakinin - American cockroach

C;Species: Periplaneta americana (American cockroach)

C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 11-Jul-1997

C;Accession: A60656

R;Veenstra, J.A.

Neuropeptides 14, 145-149, 1989

A;Title: Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockroach homologous to the leucosulfakinins.

A;Reference number: A60656; MUID:90137190; PMID:2615921

A;Accession: A60656

A;Molecule type: protein

A;Residues: 1-11 <VEE>

C;Comment: This neuropeptide stimulates hindgut contractions.

C;Keywords: amidated carboxyl end; neuropeptide; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||
Db 1 EQ 2

RESULT 27

S68637

acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 30-Jan-1998
C;Accession: S68637
R;Boschetti, N.; Brodbeck, U.
FEBS Lett. 380, 133-136, 1996
A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of a single glycosylated protein of 22 kDa.
A;Reference number: S68637; MUID:96181683; PMID:8603722
A;Accession: S68637
A;Molecule type: protein
A;Residues: 1-11 <BOS>
A;Experimental source: brain
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QK 7
||
Db 3 QK 4

RESULT 28
A33571
follistatin - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 30-Sep-1993
C;Accession: A33571
R;Gospodarowicz, D.; Lau, K.
Biochem. Biophys. Res. Commun. 165, 292-298, 1989
A;Title: Pituitary follicular cells secrete both vascular endothelial growth factor and follistatin.
A;Reference number: A33571; MUID:90073725; PMID:2590228
A;Accession: A33571
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <GOS>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 8 AK 9

RESULT 29
S54347
tubulin beta chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 07-May-1999
C;Accession: S54347
R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995

A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glial cells.
A;Reference number: S54343; MUID:95194333; PMID:7887910
A;Accession: S54347
A;Molecule type: protein
A;Residues: 1-11 <OKA>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 4 NA 5

RESULT 30

A14454
6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993
C;Accession: A14454
R;Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.
Biochem. Soc. Trans. 7, 721-723, 1979
A;Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.
A;Reference number: A14454; MUID:80004524; PMID:157899
A;Accession: A14454
A;Molecule type: protein
A;Residues: 1-11 <FOR>
C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 8 AK 9

RESULT 31

A61483
pyridoxal kinase (EC 2.7.1.35) - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C;Accession: A61483
R;Churchich, J.E.
J. Protein Chem. 9, 613-621, 1990
A;Title: Cleavage of pyridoxal kinase into two structural domains: kinetics of proteolysis monitored by emission anisotropy.
A;Reference number: A61483; MUID:91197387; PMID:2085386
A;Accession: A61483
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <CHU>
C;Keywords: homodimer; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QR 9
||
Db 10 QR 11

RESULT 32

PH1376

T antigen variant K-3 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

C;Accession: PH1376

R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.

J. Exp. Med. 176, 449-457, 1992

A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for transformed cells with point mutations within sequences encoding CTL recognition epitopes.

A;Reference number: PH1373; MUID:92364547; PMID:1380062

A;Accession: PH1376

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <LIL>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 6 KE 7

RESULT 33

PT0214

T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0214

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0214

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||

Db 8 EQ 9

RESULT 34

S53436

beta-D-galactosidase - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Aug-1995 #sequence_revision 15-May-1998 #text_change 07-May-1999

C;Accession: S53436; S53437

R;Tulsiani, D.R.P.; Skudlarek, M.D.; Araki, Y.; Orgebin-Crist, M.C.

Biochem. J. 305, 41-50, 1995

A;Title: Purification and characterization of two forms of beta-D-galactosidase from rat epididymal luminal fluid: evidence for their role in the modification of sperm plasma membrane glycoprotein(s).

A;Reference number: S53436; MUID:95126928; PMID:7826352

A;Accession: S53436

A;Molecule type: protein

A;Residues: 1-11 <TUL>

A;Experimental source: epididymal fluid

A;Note: 84K form

A;Accession: S53437

A;Molecule type: protein

A;Residues: 1-11 <TUW>

A;Experimental source: epididymal fluid

A;Note: 97K form

C;Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QR 9

||

Db 6 QR 7

RESULT 35

S65377

cytochrome-c oxidase (EC 1.9.3.1) chain VIa-H, cardiac - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999

C;Accession: S65377

R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.

A;Reference number: S65372; MUID:95324529; PMID:7601105

A;Accession: S65377

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 3 AK 4

RESULT 36

PH0941

T-cell receptor beta chain V-D-J region (clone 12) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0941
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0941
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||
Db 10 EQ 11

RESULT 37

PH0929

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0929
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0929
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||
Db 10 EQ 11

RESULT 38

PH0924

T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0924

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0924

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6

||

Db 10 EQ 11

RESULT 39

PH0919

T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0919

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0919

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

A;Note: the authors translated the codon CAG for residue 11 as Glu

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10

||

Db 7 RN 8

RESULT 40

PH0914

T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0914
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0914
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: myelin basic protein-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||
Db 10 EQ 11

RESULT 41
H84082
hypothetical protein BH3464 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: H84082
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji,
F.; Hirama, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84082
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB07183.1;
GSPDB:GN00137
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3464

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 4 KE 5

RESULT 42
S19015
hypothetical protein 11 ruvC-yebC intergenic region - Escherichia coli

C;Species: Escherichia coli
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: S19015
R;Sharples, G.J.; Lloyd, R.G.
J. Bacteriol. 173, 7711-7715, 1991
A;Title: Resolution of Holliday junctions in Escherichia coli: identification of the ruvC gene product as a 19-kilodalton protein.
A;Reference number: S19013; MUID:92041688; PMID:1657895
A;Accession: S19015
A;Molecule type: DNA
A;Residues: 1-11 <SHA>
A;Cross-references: EMBL:X59551; NID:g42172; PIDN:CAA42127.1; PID:g42174
C;Comment: This is the hypothetical translation of a sequence that was not reported as a coding sequence in the complete genome.

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 4 AK 5

RESULT 43
XAVIBH
bradykinin-potentiating peptide - halys viper
N;Alternate names: BPP
C;Species: Agkistrodon halys (halys viper)
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994
C;Accession: JC0002
R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.
Peptides 6, 339-342, 1985
A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).
A;Reference number: JC0002; MUID:86177022; PMID:3008123
A;Accession: JC0002
A;Molecule type: protein
A;Residues: 1-11 <CHI>
C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyroglutamic acid; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 44

XASNBA
bradykinin-potentiating peptide B - mamushi
C;Species: Agkistrodon blomhoffi (mamushi)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C;Accession: A01254
R;Kato, H.; Suzuki, T.
Proc. Jpn. Acad. 46, 176-181, 1970
A;Reference number: A01254
A;Accession: A01254
A;Molecule type: protein
A;Residues: 1-11 <KAT>
A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 45
ECLQ2M
tachykinin II - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995
C;Accession: S08266
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.
FEBS Lett. 261, 397-401, 1990
A;Title: Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family.
A;Reference number: S08265; MUID:90184489; PMID:2311766
A;Accession: S08266
A;Molecule type: protein
A;Residues: 1-11 <SCH>
C;Superfamily: tachykinin
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 46
SPHO
substance P - horse

C;Species: Equus caballus (domestic horse)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C;Accession: A01558
R;Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973
A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.
A;Reference number: A01558
A;Accession: A01558
A;Molecule type: protein
A;Residues: 1-11 <STU>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 1 R 1

RESULT 47
EOOCC
eleodoisin - curled octopus
C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
C;Accession: B01561; A01561
R;Anastasi, A.; Erspamer, V.
Arch. Biochem. Biophys. 101, 56-65, 1963
A;Title: The isolation and amino acid sequence of eleodoisin, the active
endecapeptide of the posterior salivary glands of Eledone.
A;Reference number: A01561
A;Accession: B01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;
secretagogue; vasodilator; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 48
A60654
substance P - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C;Accession: A60654
R;Murphy, R.
Neuropeptides 14, 105-110, 1989
A;Title: Primary amino acid sequence of guinea-pig substance P.
A;Reference number: A60654; MUID:90044685; PMID:2478925
A;Accession: A60654
A;Molecule type: protein
A;Residues: 1-11 <MUR>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 1 R 1

RESULT 49
EOOC
eledoisin - musky octopus
C;Species: Eledone moschata, Ozaena moschata (musky octopus)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998
C;Accession: A01561
R;Anastasi, A.; Erspamer, V.
Arch. Biochem. Biophys. 101, 56-65, 1963
A;Title: The isolation and amino acid sequence of eleodisin, the active
endecapeptide of the posterior salivary glands of Eledone.
A;Reference number: A01561
A;Accession: A01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;
secretagogue; vasodilator; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 50
LFTWWE
probable trpEG leader peptide - Thermus aquaticus
C;Species: Thermus aquaticus
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: S03315
R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.

Biochim. Biophys. Acta 950, 303-312, 1988
A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8
trpE and trpG.
A;Reference number: S03315; MUID:89000781; PMID:2844259
A;Accession: S03315
A;Molecule type: DNA
A;Residues: 1-11 <SAT>
A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262
A;Note: the source is designated as *Thermus thermophilus* HB8
C;Genetics:
A;Gene: trpL
C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 51
S66196
alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (Gadus
sp.) (fragment)
C;Species: Gadus sp. (cod)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998
C;Accession: S66196
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.;
Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H.
FEBS Lett. 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol
dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and
higher vertebrate class I, II, and III forms of the enzyme.
A;Reference number: S66191; MUID:95331382; PMID:7607314
A;Accession: S66196
A;Molecule type: protein
A;Residues: 1-11 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 3 R 3

RESULT 52
S68392
H⁺-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlamydomonas
reinhardtii chloroplast (fragment)
N;Alternate names: ATP synthase chain I
C;Species: chloroplast Chlamydomonas reinhardtii

C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002
C;Accession: S68392
R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995
A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal amino acid sequences of the CF(0)CF(1) subunits.
A;Reference number: S68388; MUID:96128220; PMID:8543042
A;Accession: S68392
A;Molecule type: protein
A;Residues: 1-11 <FIE>
A;Experimental source: strain CW15
C;Genetics:
A;Genome: chloroplast
C;Superfamily: H⁺-transporting ATP synthase protein 6
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 E 5
|
Db 1 E 1

RESULT 53
B49164
chromogranin-B - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C;Accession: B49164
R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.
Endocrinology 129, 3147-3156, 1991
A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides through processing at mono-, di-, or tribasic residues.
A;Reference number: A49164; MUID:92063871; PMID:1954895
A;Accession: B49164
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <NIE>
A;Note: sequence extracted from NCBI backbone (NCBIP:66370)
C;Superfamily: chromogranin B precursor

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 E 5
|
Db 4 E 4

RESULT 54
JN0023
substance P - chicken
C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C;Accession: JN0023
R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A;Reference number: JN0023; MUID:88204263; PMID:2452461
A;Accession: JN0023
A;Molecule type: protein
A;Residues: 1-11 <CON>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 1 R 1

RESULT 55
S32575
ribosomal protein S2, plastid - squawroot plastid (fragment)
C;Species: plastid Conopholis americana (squawroot)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999
C;Accession: S32575
R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.
Curr. Genet. 20, 515-518, 1991
A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of
photosynthesis in a lineage of parasitic plants.
A;Reference number: S32575; MUID:92145776; PMID:1723664
A;Accession: S32575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <TAY>
A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276
C;Genetics:
A;Gene: rps2
A;Genome: plastid
C;Superfamily: Escherichia coli ribosomal protein S2
C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 E 5
|
Db 11 E 11

RESULT 56
A40693
transgelin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Oct-1997
C;Accession: A40693
R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.
J. Cell Biol. 121, 1065-1073, 1993
A;Title: Purification and properties of transgelin: a transformation and shape
change sensitive actin-gelling protein.
A;Reference number: A40693; MUID:93273790; PMID:8501116
A;Accession: A40693
A;Molecule type: protein
A;Residues: 1-11 <SHA>
A;Experimental source: aorta
C;Comment: This protein gels actin and is down regulated by transformation or
loss of cell adherence in culture.
C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth
muscle protein SM22 homology
C;Keywords: actin binding; cytoskeleton

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 57
S00616
parasporal crystal protein, wax moth-specific - *Bacillus thuringiensis* (strain
galleriae 11-67) (fragment)
N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain
C;Species: *Bacillus thuringiensis*
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Sep-1996
C;Accession: S00616
R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.
FEBS Lett. 232, 249-251, 1988
A;Title: *Bacillus thuringiensis* ssp. *galleriae* simultaneously produces two
delta-endotoxins differing strongly in primary structure and entomocidal
activity.
A;Reference number: S00615
A;Accession: S00616
A;Molecule type: protein
A;Residues: 1-11 <CHE>
C;Comment: This toxin is effective against the larvae of *Galleria melonella*
(greater wax moth) but not those of *Lymantria dispar* (gypsy moth).
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 4 A 4

RESULT 58
A57458
gene Gax protein - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999
C;Accession: A57458
R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.
Mol. Cell. Biol. 15, 4272-4281, 1995
A;Title: Regulation of Gax homeobox gene transcription by a combination of positive factors including myocyte-specific enhancer factor 2.
A;Reference number: A57458; MUID:95349593; PMID:7623821
A;Accession: A57458
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
A;Cross-references: GB:S79168; NID:g1050991
C;Genetics:
A;Gene: Gax
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 E 5
|
Db 2 E 2

RESULT 59
A26930
ermG leader peptide 1 - *Bacillus sphaericus*
C;Species: *Bacillus sphaericus*
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 24-Sep-1999
C;Accession: A26930
R;Monod, M.; Mohan, S.; Dubnau, D.
J. Bacteriol. 169, 340-350, 1987
A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance element from *Bacillus sphaericus*.
A;Reference number: A91840; MUID:87083389; PMID:3025178
A;Accession: A26930
A;Molecule type: DNA
A;Residues: 1-11 <MON>
A;Cross-references: GB:M15332; NID:g142881; PIDN:AAA22417.1; PID:g142882
C;Superfamily: unassigned leader peptides

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 N 10
|
Db 2 N 2

RESULT 60

D60409

kassinin-like peptide K-III - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: D60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: D60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 61

F60409

substance P-like peptide II - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: F60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: F60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 62

E60409

substance P-like peptide I - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: E60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: E60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	6	Q	6
Db	1	Q	1

RESULT 63

YHRT

morphogenetic neuropeptide - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: A01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator by the authors, because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 64

YHHU

morphogenetic neuropeptide - human

C;Species: Homo sapiens (man)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B01427; A01427

R;Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981

A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.

A;Reference number: A93266; MUID:82035850; PMID:7290191

A;Accession: B01427

A;Molecule type: protein

A;Residues: 1-11 <BOD>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide

F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 65

YHBO

morphogenetic neuropeptide - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: C01427; A01427

R;Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.
A;Reference number: A93266; MUID:82035850; PMID:7290191
A;Accession: C01427
A;Molecule type: protein
A;Residues: 1-11 <BOD>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has been found in mammalian intestine and hypothalamus.
C;Superfamily: unassigned animal peptides
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 66
YHXAE
morphogenetic neuropeptide - sea anemone (*Anthopleura elegantissima*)
N;Alternate names: head activator
C;Species: *Anthopleura elegantissima*
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A93900; A01427
R;Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A;Reference number: A93900
A;Accession: A93900
A;Molecule type: protein
A;Residues: 1-11 <SCH>
R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.
A;Reference number: A91296; MUID:82050803; PMID:7297679
A;Contents: annotation; synthesis
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 67

YHJFHY

morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator

C;Species: Hydra attenuata

C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C;Accession: B93900; A01427

R;Schaller, H.C.; Bodenmuller, H.

Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.

A;Reference number: A93900

A;Accession: B93900

A;Molecule type: protein

A;Residues: 1-11 <SCH>

R;Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.

FEBS Lett. 131, 317-321, 1981

A;Title: Synthesis of a new neuropeptide, the head activator from hydra.

A;Reference number: A91296; MUID:82050803; PMID:7297679

A;Contents: annotation; synthesis

A;Note: the synthetic peptide was identical with the natural peptide in chemical structure and biological activity

C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator because it induced head-specific growth and differentiation in this animal. It has also been found in mammalian intestine and hypothalamus.

C;Superfamily: unassigned animal peptides

C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 68

A61365

phyllokinin - Rohde's leaf frog

N;Alternate names: bradykinyl-isoleucyl-tyrosine O-sulfate

C;Species: Phylomedusa rohdei (Rohde's leaf frog)

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000

C;Accession: A61365

R;Anastasi, A.; Bertaccini, G.; Erspamer, V.

Br. J. Pharmacol. 27, 479-485, 1966

A;Title: Pharmacological data on phyllokinin (bradykinyl-isoleucyl-tyrosine O-sulphate) and bradykinyl-isoleucyl-tyrosine.

A;Reference number: A61365; MUID:67179312; PMID:5970899

A;Accession: A61365

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: unassigned animal peptides

C;Keywords: sulfoprotein

F;11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 1 R 1

RESULT 69

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: Megascolia flavifrons (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp Megascolia flavifrons.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of Megascolia flavifrons.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein

A;Residues: 1-11 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 1 R 1

RESULT 70

S23308

substance P - rainbow trout

C;Species: *Oncorhynchus mykiss* (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neuropeptide-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 71

S23306

substance P - Atlantic cod

C;Species: *Gadus morhua* (Atlantic cod)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neuropeptide-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23306

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 72

B60409

kassinin-like peptide K-I - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C;Accession: B60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: B60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

A;Note: this peptide was also found in a deamidated form

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 73

C60409

kassinin-like peptide K-II - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C;Accession: C60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: C60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
A;Note: this peptide was also found in a deamidated form
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 74
S07207
Crinia-angiotensin, skin - frog (Crinia georgiana)
C;Species: Crinia georgiana
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000
C;Accession: S07207
R;Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
Experientia 35, 1132-1133, 1979
A;Title: Amino acid composition and sequence of crinia-angiotensin, an
angiotensin II-like endecapeptide from the skin of the Australian frog Crinia
georgiana.
A;Reference number: S07207; MUID:80024575; PMID:488254
A;Accession: S07207
A;Molecule type: protein
A;Residues: 1-11 <ERS>
C;Superfamily: unassigned animal peptides

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 A 1

RESULT 75
S07201
physalaemin - frog (Physalaemus fuscomaculatus)
C;Species: Physalaemus fuscomaculatus
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07201
R;Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.
Experientia 20, 489-490, 1964
A;Title: Structure and pharmacological actions of physalaemin, the main active
polypeptide of the skin of Physalaemus fuscomaculatus.
A;Reference number: S07201; MUID:66076612; PMID:5857249
A;Accession: S07201
A;Molecule type: protein

A;Residues: 1-11 <ERS>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

Search completed: April 8, 2004, 15:49:28
Job time : 8.61538 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds
(without alignments)
95.432 Million cell updates/sec

Title: US-09-787-443A-20

Perfect score: 11

Sequence: 1 AKKKEQKQRNA 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB ID	Description
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1	4	36.4	11	10	US-09-876-904A-273	Sequence 273, App
2	4	36.4	11	10	US-09-876-904A-354	Sequence 354, App
3	4	36.4	11	14	US-10-355-975-33	Sequence 33, Appl
4	4	36.4	11	14	US-10-304-443-91	Sequence 91, Appl
5	4	36.4	11	14	US-10-020-269-34	Sequence 34, Appl
6	3	27.3	11	9	US-09-765-527-206	Sequence 206, App
7	3	27.3	11	9	US-09-879-936-10	Sequence 10, Appl
8	3	27.3	11	9	US-09-192-854-123	Sequence 123, App
9	3	27.3	11	9	US-09-780-662A-15	Sequence 15, Appl
10	3	27.3	11	9	US-09-881-490-181	Sequence 181, App
11	3	27.3	11	9	US-09-898-461-8	Sequence 8, Appli
12	3	27.3	11	9	US-09-938-315-105	Sequence 105, App
13	3	27.3	11	9	US-09-988-899-1	Sequence 1, Appli
14	3	27.3	11	9	US-09-813-333-10	Sequence 10, Appl
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16	3	27.3	11	9	US-09-966-871-4	Sequence 4, Appli
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19	3	27.3	11	9	US-09-969-192-19	Sequence 19, Appl
20	3	27.3	11	9	US-09-968-561A-220	Sequence 220, App
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23	3	27.3	11	9	US-09-805-301-43	Sequence 43, Appl
24	3	27.3	11	9	US-09-805-301-99	Sequence 99, Appl
25	3	27.3	11	9	US-09-201-936-43	Sequence 43, Appl
26	3	27.3	11	10	US-09-999-724-76	Sequence 76, Appl
27	3	27.3	11	10	US-09-906-393A-9	Sequence 9, Appli
28	3	27.3	11	10	US-09-882-291-55	Sequence 55, Appl
29	3	27.3	11	10	US-09-882-291-64	Sequence 64, Appl
30	3	27.3	11	10	US-09-876-904A-25	Sequence 25, Appl
31	3	27.3	11	10	US-09-876-904A-77	Sequence 77, Appl
32	3	27.3	11	10	US-09-876-904A-200	Sequence 200, App
33	3	27.3	11	10	US-09-876-904A-237	Sequence 237, App
34	3	27.3	11	10	US-09-876-904A-362	Sequence 362, App
35	3	27.3	11	10	US-09-876-904A-363	Sequence 363, App
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37	3	27.3	11	10	US-09-876-904A-373	Sequence 373, App
38	3	27.3	11	10	US-09-876-904A-434	Sequence 434, App
39	3	27.3	11	10	US-09-876-904A-542	Sequence 542, App
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41	3	27.3	11	10	US-09-876-904A-591	Sequence 591, App
42	3	27.3	11	10	US-09-876-904A-597	Sequence 597, App
43	3	27.3	11	10	US-09-820-053A-113	Sequence 113, App
44	3	27.3	11	10	US-09-820-053A-139	Sequence 139, App
45	3	27.3	11	10	US-09-530-139-1	Sequence 1, Appli
46	3	27.3	11	10	US-09-852-910-55	Sequence 55, Appl
47	3	27.3	11	10	US-09-852-910-160	Sequence 160, App
48	3	27.3	11	10	US-09-852-910-254	Sequence 254, App
49	3	27.3	11	10	US-09-994-487-3	Sequence 3, Appli
50	3	27.3	11	10	US-09-791-524-15	Sequence 15, Appl
51	3	27.3	11	10	US-09-968-744A-220	Sequence 220, App
52	3	27.3	11	10	US-09-854-248-20	Sequence 20, Appl
53	3	27.3	11	11	US-09-077-439A-16	Sequence 16, Appl
54	3	27.3	11	11	US-09-737-476B-3	Sequence 3, Appli
55	3	27.3	11	12	US-09-968-561A-220	Sequence 220, App
56	3	27.3	11	12	US-10-362-527-83	Sequence 83, Appl

57	3	27.3	11	12	US-10-362-527-84	Sequence 84, Appl
58	3	27.3	11	12	US-10-457-082-3	Sequence 3, Appli
59	3	27.3	11	12	US-10-458-860-4	Sequence 4, Appli
60	3	27.3	11	12	US-10-653-595-458	Sequence 458, App
61	3	27.3	11	12	US-10-239-103-10	Sequence 10, Appl
62	3	27.3	11	12	US-10-156-527-5	Sequence 5, Appli
63	3	27.3	11	12	US-10-156-527-12	Sequence 12, Appl
64	3	27.3	11	13	US-10-039-645-4	Sequence 4, Appli
65	3	27.3	11	13	US-10-044-703-10	Sequence 10, Appl
66	3	27.3	11	14	US-10-108-795-28	Sequence 28, Appl
67	3	27.3	11	14	US-10-108-795-29	Sequence 29, Appl
68	3	27.3	11	14	US-10-115-365-28	Sequence 28, Appl
69	3	27.3	11	14	US-10-115-365-29	Sequence 29, Appl
70	3	27.3	11	14	US-10-146-574-27	Sequence 27, Appl
71	3	27.3	11	14	US-10-116-391-10	Sequence 10, Appl
72	3	27.3	11	14	US-10-139-084-4	Sequence 4, Appli
73	3	27.3	11	14	US-10-075-869-26	Sequence 26, Appl
74	3	27.3	11	14	US-10-109-171-113	Sequence 113, App
75	3	27.3	11	14	US-10-109-171-139	Sequence 139, App
76	3	27.3	11	14	US-10-251-364-12	Sequence 12, Appl
77	3	27.3	11	14	US-10-087-286-8	Sequence 8, Appli
78	3	27.3	11	14	US-10-053-975A-4	Sequence 4, Appli
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80	3	27.3	11	14	US-10-265-071-21	Sequence 21, Appl
81	3	27.3	11	14	US-10-322-210-29	Sequence 29, Appl
82	3	27.3	11	14	US-10-322-210-30	Sequence 30, Appl
83	3	27.3	11	14	US-10-025-966A-21	Sequence 21, Appl
84	3	27.3	11	14	US-10-116-212-28	Sequence 28, Appl
85	3	27.3	11	14	US-10-116-212-29	Sequence 29, Appl
86	3	27.3	11	14	US-10-182-303-15	Sequence 15, Appl
87	3	27.3	11	14	US-10-050-200-41	Sequence 41, Appl
88	3	27.3	11	14	US-10-315-515-22	Sequence 22, Appl
89	3	27.3	11	14	US-10-226-629A-22	Sequence 22, Appl
90	3	27.3	11	14	US-10-226-629A-36	Sequence 36, Appl
91	3	27.3	11	14	US-10-403-340-17	Sequence 17, Appl
92	3	27.3	11	14	US-10-304-443-29	Sequence 29, Appl
93	3	27.3	11	14	US-10-304-443-30	Sequence 30, Appl
94	3	27.3	11	14	US-10-304-443-118	Sequence 118, App
95	3	27.3	11	14	US-10-105-232-379	Sequence 379, App
96	3	27.3	11	14	US-10-105-232-407	Sequence 407, App
97	3	27.3	11	14	US-10-105-232-452	Sequence 452, App
98	3	27.3	11	14	US-10-105-232-524	Sequence 524, App
99	3	27.3	11	14	US-10-082-014-94	Sequence 94, Appl
100	3	27.3	11	14	US-10-161-791-105	Sequence 105, App

ALIGNMENTS

RESULT 1

US-09-876-904A-273

; Sequence 273, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila sp.
; FEATURE:
; OTHER INFORMATION: Recombination repair protein 1
US-09-876-904A-273

Query Match 36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KKKE 5
Db 6 KKKE 9

RESULT 2
US-09-876-904A-354
; Sequence 354, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 354
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human ATF-3 (in basic region that binds DNA)
US-09-876-904A-354

Query Match 36.4%; Score 4; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKKE 5
|||
Db 6 KKKE 9

RESULT 3

US-10-355-975-33

; Sequence 33, Application US/10355975
; Publication No. US20030162277A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/10/355,975
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US/09/579,664B
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide

US-10-355-975-33

Query Match 36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKKE 5
|||
Db 2 KKKE 5

RESULT 4

US-10-304-443-91

; Sequence 91, Application US/10304443
; Publication No. US20030170229A1
; GENERAL INFORMATION:
; APPLICANT: Smithkline Beecham Biologicals s.a.
; APPLICANT: Peptide Therapeutics Ltd.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45173CIP
; CURRENT APPLICATION NUMBER: US/10/304,443
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US/09/698,906A
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 11

; TYPE: PRT
; ORGANISM: Human peptide sequence
US-10-304-443-91

Query Match 36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQRN 10
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Db 3 KQRN 6

RESULT 5

US-10-020-269-34

; Sequence 34, Application US/10020269
; Publication No. US20030175310A1
; GENERAL INFORMATION:
; APPLICANT: Mitchell, William M.
; APPLICANT: Stratton, Charles W.
; TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE: VDB98-01
; CURRENT APPLICATION NUMBER: US/10/020,269
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/025,596
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/023,921
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-14
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae

US-10-020-269-34

Query Match 36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKKK 4
||||
Db 3 AKKK 6

RESULT 6

US-09-765-527-206

; Sequence 206, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.350"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-Terminus is Amidated."
SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-765-527-206

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
Pb 1 KKK 3

RESULT 7
US-09-879-936-10
; Sequence 10, Application US/09879936
; Patent No. US20020045564A1
; GENERAL INFORMATION:
; APPLICANT: Van Eyk, Jennifer E.
; APPLICANT: Mak, Alan S.

; APPLICANT: Cote, Graham P.
; TITLE OF INVENTION: Methods of Modulating Muscle Contraction
; FILE REFERENCE: 1997-021-03US
; CURRENT APPLICATION NUMBER: US/09/879,936
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/050,478
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 60/089,505
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(11)
; OTHER INFORMATION: Residues 423 to 433 of chicken gizzard caldesmon
; NAME/KEY: PEPTIDE
; LOCATION: (11)
; OTHER INFORMATION: Targeted Ser phospho-amino acid
US-09-879-936-10

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 7 AKK 9

RESULT 8
US-09-192-854-123
; Sequence 123, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-123

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
|||
Db 7 KQR 9

RESULT 9
US-09-780-662A-15
; Sequence 15, Application US/09780662A
; Patent No. US20020076741A1
; GENERAL INFORMATION:
; APPLICANT: Burroughs-Tencza, Sarah
; TITLE OF INVENTION: Biosensor for Anthrax
; FILE REFERENCE: MBHB00-126-A
; CURRENT APPLICATION NUMBER: US/09/780,662A
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Synthetic peptide sequence
US-09-780-662A-15

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QRN 10
|||
Db 3 QRN 5

RESULT 10
US-09-881-490-181
; Sequence 181, Application US/09881490
; Patent No. US20020077298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th FloorDrive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/881,490
FILING DATE: 14-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/119,858
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-94
APPLICATION NUMBER: 08/093,202
FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: "XMP.350"
FEATURE:
NAME/KEY: Modified-site
LOCATION: C-Terminus
OTHER INFORMATION: /label= Amidation
/note= "The C-Terminus is Amidated"
SEQUENCE DESCRIPTION: SEQ ID NO: 181:
US-09-881-490-181
Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	KKK	4
Pb	1	KKK	3

RESULT 11
US-09-898-461-8

; Sequence 8, Application US/09898461
; Patent No. US20020090709A1
; GENERAL INFORMATION:
; APPLICANT: Begent, Richard HJ
; APPLICANT: Chester, Kerry
; APPLICANT: Minton, Nigel P
; APPLICANT: Rees, Anthony R
; APPLICANT: Sharma, Surinder K
; APPLICANT: Spencer, Daniel IR
; TITLE OF INVENTION: Modified carboxypeptidase enzymes and their use
; FILE REFERENCE: 620-150
; CURRENT APPLICATION NUMBER: US/09/898,461
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: US 60/216,689
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: myc tag
US-09-898-461-8

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 12
US-09-938-315-105
; Sequence 105, Application US/09938315
; Patent No. US20020091085A1
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; SPARKS, ANDREW B.
; THORN, JUDITH M.
; QUILLIAM, LAWRENCE A.
; DER, CHANNING J.
; TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,315
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-09-938-315-105

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
 |||
Db 1 EQK 3

RESULT 13

US-09-988-899-1

; Sequence 1, Application US/09988899
; Patent No. US20020102613A1
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, HENDRICUS R.J.M.
; TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
; FILE REFERENCE: DX/003 CON
; CURRENT APPLICATION NUMBER: US/09/988,899
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/US00/13682
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 99201558.6
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide
US-09-988-899-1

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 14

US-09-813-333-10

; Sequence 10, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis

US-09-813-333-10

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 9 EQK 11

RESULT 15

US-09-974-592-17

; Sequence 17, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053

; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Based on Homo sapiens sequence
US-09-974-592-17

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 16

US-09-966-871-4

; Sequence 4, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; TITLE OF INVENTION: Alterations in Signaling
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-4

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 17

US-09-833-079-2

; Sequence 2, Application US/09833079

; Patent No. US20020142008A1
; GENERAL INFORMATION:
; APPLICANT: O'HANLEY, PETER
; APPLICANT: DENICH, KENNETH
; APPLICANT: SCHMIDT, M. ALEXANDER
; TITLE OF INVENTION: IMMUNOGENIC PILI PRESENTING FOREIGN PEPTIDES, THEIR
; TITLE OF INVENTION: PRODUCTION AND USE
; FILE REFERENCE: 050939/0104
; CURRENT APPLICATION NUMBER: US/09/833,079
; CURRENT FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-833-079-2

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
Db 8 AKK 10

RESULT 18
US-09-833-079-17
; Sequence 17, Application US/09833079
; Patent No. US20020142008A1
; GENERAL INFORMATION:
; APPLICANT: O'HANLEY, PETER
; APPLICANT: DENICH, KENNETH
; APPLICANT: SCHMIDT, M. ALEXANDER
; TITLE OF INVENTION: IMMUNOGENIC PILI PRESENTING FOREIGN PEPTIDES, THEIR
; TITLE OF INVENTION: PRODUCTION AND USE
; FILE REFERENCE: 050939/0104
; CURRENT APPLICATION NUMBER: US/09/833,079
; CURRENT FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-833-079-17

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 8 AKK 10

RESULT 19

US-09-969-192-19

; Sequence 19, Application US/09969192
; Patent No. US20020151027A1

; GENERAL INFORMATION:

; APPLICANT: WICKHAM, THOMAS J.
; ROELVINK, PETRUS W.
; KOVESDI, IMRE

; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; CONSTRAINED PEPTIDE MOTIFS

; NUMBER OF SEQUENCES: 80

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/969,192
; FILING DATE: 01-Oct-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 9-455061
; FILING DATE: 06-DEC-1999
; APPLICATION NUMBER: US 9-130225
; FILING DATE: 06-AUG-1998
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Hefner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 213564

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-969-192-19

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4

|||
Db 3 KKK 5

RESULT 20
US-09-968-561A-220
; Sequence 220, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-220

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
|||
Db 7 KQR 9

RESULT 21
US-09-858-332-13
; Sequence 13, Application US/09858332
; Patent No. US20020164718A1
; GENERAL INFORMATION:
; APPLICANT: Tchaga, Grigory S.
; APPLICANT: Jokhadze, George
; TITLE OF INVENTION: Metal Ion Affinity Tags and Methods for
; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: CLON056CIP
; CURRENT APPLICATION NUMBER: US/09/858,332
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 09/404,017
; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,867
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-858-332-13

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 22

US-09-805-301-5

; Sequence 5, Application US/09805301

; Patent No. US20020173456A1

; GENERAL INFORMATION:

; APPLICANT: Smith, Louis C.
; Sparrow, James T.
; Hauer, Jochen
; Mims, Martha P.

; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; MACROMOLECULE DELIVERY

; NUMBER OF SEQUENCES: 139

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 6.0

; SOFTWARE: Word Perfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/805,301

; FILING DATE: 12-Mar-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/584,043

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 217/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-805-301-5

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 1 KKK 3

RESULT 23

US-09-805-301-43

; Sequence 43, Application US/09805301
; Patent No. US20020173456A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Louis C.
; Sparrow, James T.
; Hauer, Jochen
; Mims, Martha P.
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; MACROMOLECULE DELIVERY
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 6.0
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/805,301
; FILING DATE: 12-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/584,043
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally occurring amino acid and analogues thereof.
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-805-301-43

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4
|||
Db 1 KKK 3

RESULT 24
US-09-805-301-99
Sequence 99, Application US/09805301
Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1

;

CURRENT APPLICATION DATA:

;

APPLICATION NUMBER: US/09/805,301

;

FILING DATE: 12-Mar-2001

;

CLASSIFICATION: <Unknown>

;

PRIOR APPLICATION DATA:

;

APPLICATION NUMBER: 08/584,043

;

FILING DATE: <Unknown>

;

ATTORNEY/AGENT INFORMATION:

;

NAME: Warburg, Richard J.

;

REGISTRATION NUMBER: 32,327

;

REFERENCE/DOCKET NUMBER: 217/189

;

TELECOMMUNICATION INFORMATION:

;

TELEPHONE: (213) 489-1600

;

TELEFAX: (213) 955-0440

;

TELEX: 67-3510

;

INFORMATION FOR SEQ ID NO: 99:

;

SEQUENCE CHARACTERISTICS:

;

LENGTH: 11 amino acids

;

TYPE: amino acid

;

STRANDEDNESS: single

;

TOPOLOGY: linear

;

MOLECULE TYPE: peptide

;

SEQUENCE DESCRIPTION: SEQ ID NO: 99:

US-09-805-301-99

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 1 KKK 3

RESULT 25

US-09-201-936-43

;

Sequence 43, Application US/09201936

;

Publication No. US20020187946A1

;

GENERAL INFORMATION:

;

APPLICANT: Korneluk, Robert G.

;

APPLICANT: MacKenzie, Alexander E.

;

APPLICANT: Baird, Stephen

;

APPLICANT: Liston, Peter

;

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

;

TITLE OF INVENTION: PROBES, AND DETECTION METHODS

;

FILE REFERENCE: 07891/003003

;

CURRENT APPLICATION NUMBER: US/09/201,936

;

CURRENT FILING DATE: 1998-12-01

;

EARLIER APPLICATION NUMBER: 09/011,356

;

EARLIER FILING DATE: 1998-02-04

;

EARLIER APPLICATION NUMBER: PCT/IB96/01022

;

EARLIER FILING DATE: 1996-08-05

;

EARLIER APPLICATION NUMBER: 08/576,956

;

EARLIER FILING DATE: 1995-12-22

;

EARLIER APPLICATION NUMBER: 08/511,485

;

EARLIER FILING DATE: 1995-08-04

;

NUMBER OF SEQ ID NOS: 45

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic based on viral sequence
US-09-201-936-43

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 26

US-09-999-724-76

; Sequence 76, Application US/09999724
; Publication No. US20030022355A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
; FILE REFERENCE: 212960
; CURRENT APPLICATION NUMBER: US/09/999,724
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/101,751
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic

US-09-999-724-76

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 3 KKK 5

RESULT 27

US-09-906-393A-9

; Sequence 9, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-906-393A-9

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3

|||

Db 3 AKK 5

RESULT 28

US-09-882-291-55

; Sequence 55, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
sequence

US-09-882-291-55

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 6 KKK 8

RESULT 29

US-09-882-291-64

; Sequence 64, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1el Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence

US-09-882-291-64

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 6 KKK 8

RESULT 30

US-09-876-904A-25

; Sequence 25, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic SV40 large
T
; OTHER INFORMATION: protein
US-09-876-904A-25

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 5 KKK 7

RESULT 31

US-09-876-904A-77

; Sequence 77, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
crosslinked
; OTHER INFORMATION: to bovine serum albumin
US-09-876-904A-77

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 6 KKK 8

RESULT 32

US-09-876-904A-200

; Sequence 200, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 200
; LENGTH: 11
; TYPE: PRT
; ORGANISM: *Saccharomyces cerevisiae*
; FEATURE:
; OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-200

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 33
US-09-876-904A-237
; Sequence 237, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 237
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US-09-876-904A-237

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
|||
Db 7 KKE 9

RESULT 34

US-09-876-904A-362

; Sequence 362, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 362
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Murine LEF-1.

US-09-876-904A-362

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 2 KKK 4

RESULT 35

US-09-876-904A-363

; Sequence 363, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 363
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TCF-1 alpha.
US-09-876-904A-363

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 2 KKK 4

RESULT 36

US-09-876-904A-364

; Sequence 364, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 364
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TCF-1
US-09-876-904A-364

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 2 KKK 4

RESULT 37

US-09-876-904A-373
; Sequence 373, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 373
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MBP-1 (class I MHC enhancer binding protein
; OTHER INFORMATION: 1) mw 200 kD.
US-09-876-904A-373

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 3 KKK 5

RESULT 38
US-09-876-904A-434
; Sequence 434, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 434
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila sp.

; FEATURE:
; OTHER INFORMATION: Drosophila ultrabiothorax protein (from the
; OTHER INFORMATION: conserved 61 amino acid homeodomain segment only).
US-09-876-904A-434

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
|||
Db 8 KKE 10

RESULT 39

US-09-876-904A-542

; Sequence 542, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 542
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human S6 ribosomal protein (homologous to yeast
; OTHER INFORMATION: S10).
US-09-876-904A-542

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
|||
Db 3 KQR 5

RESULT 40

US-09-876-904A-544

; Sequence 544, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 544
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: Rat L17 ribosomal protein (184 aas).
US-09-876-904A-544

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 1 KKK 3

RESULT 41
US-09-876-904A-591
; Sequence 591, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 591
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Trout testis H1 (194
aa).
US-09-876-904A-591

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 42

US-09-876-904A-597

; Sequence 597, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 597
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Parechinus angulosus
; FEATURE:
; OTHER INFORMATION: Sea urchin Parechinus angulosus sperm H1 (248 aa).

US-09-876-904A-597

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 1 AKK 3

RESULT 43

US-09-820-053A-113

; Sequence 113, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 11

; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-113

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 9 AKK 11

RESULT 44

US-09-820-053A-139

; Sequence 139, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-139

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 8 AKK 10

RESULT 45

US-09-530-139-1

; Sequence 1, Application US/09530139
; Publication No. US20030092892A1
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN

; APPLICANT: LEDEBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOGT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Suitable peptide
; OTHER INFORMATION: linking group
US-09-530-139-1

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 46
US-09-852-910-55
; Sequence 55, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-852-910-55

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QRN 10

|||
Db 2 QRN 4

RESULT 47
US-09-852-910-160
; Sequence 160, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 160
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: G alpha t library peptide
US-09-852-910-160

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QRN 10
|||
Db 2 QRN 4

RESULT 48
US-09-852-910-254
; Sequence 254, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 254
; LENGTH: 11

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: G11 library peptide
US-09-852-910-254

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QRN 10
|||
Db 2 QRN 4

RESULT 49

US-09-994-487-3

; Sequence 3, Application US/09994487
; Publication No. US20030099954A1
; GENERAL INFORMATION:
; APPLICANT: Miltényi, Stefan
; APPLICANT: Kohler, Matthias
; TITLE OF INVENTION: Apparatus and method for modification of
; TITLE OF INVENTION: magnetically immobilized biomolecules
; FILE REFERENCE: MILT004
; CURRENT APPLICATION NUMBER: US/09/994,487
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-994-487-3

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 50

US-09-791-524-15

; Sequence 15, Application US/09791524
; Publication No. US20030143209A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of
Heterologous Genes
; FILE REFERENCE: A3319A

; CURRENT APPLICATION NUMBER: US/09/791,524
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/09828
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524-15

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
 |||
Db 3 KKK 5

RESULT 51

US-09-968-744A-220

; Sequence 220, Application US/09968744A
; Publication No. US20030148372A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-744A-220

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
 |||

Db

7 KQR 9

RESULT 52

US-09-854-248-20

; Sequence 20, Application US/09854248

; Publication No. US20030175247A1

; GENERAL INFORMATION:

; APPLICANT: Salgaller, Michael L.

; APPLICANT: Boynton, Alton L.

; TITLE OF INVENTION: METHOD TO INCREASE CLASS I PRESENTATION OF EXOGENOUS

; TITLE OF INVENTION: ANTIGENS BY HUMAN DENDRITIC CELLS

; FILE REFERENCE: 20093-8-1US

; CURRENT APPLICATION NUMBER: US/09/854,248

; CURRENT FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 60/203,758

; PRIOR FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-248-20

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5

|||

Db 9 KKE 11

RESULT 53

US-09-077-439A-16

; Sequence 16, Application US/09077439A

; Publication No. US20030202989A1

; GENERAL INFORMATION:

; APPLICANT: Collier, R. John

; APPLICANT: Blanke, Steven R.

; APPLICANT: Milne, Jill C.

; APPLICANT: Benson, Ericka L.

; APPLICANT: Ballard, Jimmy D.

; APPLICANT: Starnbach, Michael N.

; TITLE OF INVENTION: Use of Toxin Peptides and/or Affinity

; TITLE OF INVENTION: Handles for Delivering Compounds into Cells

; FILE REFERENCE: 00246/187002

; CURRENT APPLICATION NUMBER: US/09/077,439A

; CURRENT FILING DATE: 1999-04-08

; PRIOR APPLICATION NUMBER: PCT/US96/20463

; PRIOR FILING DATE: 1996-12-13

; PRIOR APPLICATION NUMBER: US 60/019,275

; PRIOR FILING DATE: 1996-06-07

; PRIOR APPLICATION NUMBER: US 60/008,518

; PRIOR FILING DATE: 1995-12-13

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Protein
US-09-077-439A-16

Query Match 27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 1 KKK 3

RESULT 54

US-09-737-476B-3

; Sequence 3, Application US/09737476B
; Publication No. US20030208797A1
; GENERAL INFORMATION:
; APPLICANT: Leo G.J. FRENKEN
; APPLICANT: Cornelis P.E. van der LOGT
; APPLICANT: Vin-Miin TEH
; APPLICANT: Martine E. VERHOEYEN
; APPLICANT: Joy E. WILKINSON
; APPLICANT: Stephen A. JOBLING
; TITLE OF INVENTION: Production of Antibodies
; FILE REFERENCE: PNK/060113/0275850 - T7060C
; CURRENT APPLICATION NUMBER: US/09/737,476B
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: EP 99310188.0
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: MS Word
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: myc linker
US-09-737-476B-3

Query Match 27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 55

US-09-968-561A-220

; Sequence 220, Application US/09968561A

; Publication No. US20040038291A2
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 220
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-220

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQR 9
 |||
Db 7 KQR 9

RESULT 56
US-10-362-527-83
; Sequence 83, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals Y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 83
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-527-83

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 6 EQK 8

RESULT 57

US-10-362-527-84

; Sequence 84, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals Y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-527-84

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 4 EQK 6

RESULT 58

US-10-457-082-3

; Sequence 3, Application US/10457082
; Publication No. US20040033585A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation

; TITLE OF INVENTION: FLEXIBLE VACCINE ASSEMBLY AND VACCINE DELIVERY PLATFORM
; FILE REFERENCE: N8630
; CURRENT APPLICATION NUMBER: US/10/457,082
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/386,921
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,795
; PRIOR FILING DATE: 2002-09-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human antibody
US-10-457-082-3

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 1 EQK 3

RESULT 59
US-10-458-860-4
; Sequence 4, Application US/10458860
; Publication No. US20040049800A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Rapid Methods For Assessing Therapeutic
; TITLE OF INVENTION: Activity Using Animals Expressing Constitutively Active
G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: 00398/517002
; CURRENT APPLICATION NUMBER: US/10/458,860
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/388,450
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic fragment
US-10-458-860-4

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||

Db 2 EQK 4

RESULT 60
US-10-653-595-458
; Sequence 458, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: PZ027P1C1
; CURRENT APPLICATION NUMBER: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 458
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-653-595-458

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 7 KKK 9

RESULT 61
US-10-239-103-10
; Sequence 10, Application US/10239103
; Publication No. US20040057961A1
; GENERAL INFORMATION:
; APPLICANT: Brown University Research Foundation

; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004-061
; CURRENT APPLICATION NUMBER: US/10/239,103
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 09/813,333
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-239-103-10

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 9 EQK 11

RESULT 62

US-10-156-527-5

; Sequence 5, Application US/10156527
; Publication No. US20040063628A1
; GENERAL INFORMATION:
; APPLICANT: PICCARIELLO, THOMAS
; APPLICANT: KIRK, RANDAL
; APPLICANT: OLON, LAWRENCE
; TITLE OF INVENTION: ACTIVE AGENT DELIVERY SYSTEMS AND METHODS FOR PROTECTING
AND
; TITLE OF INVENTION: ADMINISTERING ACTIVE AGENTS
; FILE REFERENCE: 54719.000063
; CURRENT APPLICATION NUMBER: US/10/156,527
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 09/986,426
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 09/411,238
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 09/265,415
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 09/642,820
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/987,458
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/988,071
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/988,034
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/933,708
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/43089

; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/43117
; PRIOR FILING DATE: 2001-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-156-527-5

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	KKK	4
Db	1	KKK	3

RESULT 63

US-10-156-527-12

; Sequence 12, Application US/10156527
; Publication No. US20040063628A1
; GENERAL INFORMATION:
; APPLICANT: PICCARIELLO, THOMAS
; APPLICANT: KIRK, RANDAL
; APPLICANT: OLON, LAWRENCE
; TITLE OF INVENTION: ACTIVE AGENT DELIVERY SYSTEMS AND METHODS FOR PROTECTING
AND
; TITLE OF INVENTION: ADMINISTERING ACTIVE AGENTS
; FILE REFERENCE: 54719.000063
; CURRENT APPLICATION NUMBER: US/10/156,527
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 09/986,426
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 09/411,238
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 09/265,415
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 09/642,820
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/987,458
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/988,071
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/988,034
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/933,708
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/43089
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/43117

; PRIOR FILING DATE: 2001-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: this peptide may encompass 4-11 residues according to the
; OTHER INFORMATION: specification as filed
US-10-156-527-12

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
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Db 1 KKK 3

RESULT 64
US-10-039-645-4
; Sequence 4, Application US/10039645
; Publication No. US20020147170A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; TITLE OF INVENTION: and No. US20020147170A1functional Receptors as No.
US20020147170A1el Therapeutic Agents
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-645-4

Query Match 27.3%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK .7
 |||
Db 2 EQK 4

RESULT 65
US-10-044-703-10
; Sequence 10, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-10

Query Match 27.3%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 EQK 7
|||
Db 9 EQK 11

RESULT 66
US-10-108-795-28
; Sequence 28, Application US/10108795
; Publication No. US20030033633A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/108,795
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717089.8
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-10-108-795-28

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 67

US-10-108-795-29

; Sequence 29, Application US/10108795
; Publication No. US20030033633A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/108,795
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717089.8
; PRIOR FILING DATE: 1997-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide

US-10-108-795-29

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 68

US-10-115-365-28

; Sequence 28, Application US/10115365
; Publication No. US20030074694A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/115,365
; CURRENT FILING DATE: 2002-04-03

; PRIOR APPLICATION NUMBER: 09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-10-115-365-28

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 69

US-10-115-365-29

; Sequence 29, Application US/10115365
; Publication No: US20030074694A1
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A
; APPLICANT: Millward, Thomas A
; TITLE OF INVENTION: Calcium Regulated Kinase
; FILE REFERENCE: 30110
; CURRENT APPLICATION NUMBER: US/10/115,365
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/133,062
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: GB 9717499.9
; PRIOR FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic peptide
; OTHER INFORMATION: internal peptide
US-10-115-365-29

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 3 AKK 5

RESULT 70

US-10-146-574-27

; Sequence 27, Application US/10146574

; Publication No. US20030077246A1

; GENERAL INFORMATION:

; APPLICANT: Jing, Shuqian

; APPLICANT: Welcher, Andrew A

; APPLICANT: Boedigheimer, Michael J

; APPLICANT: Shu, Junyan

; APPLICANT: Gary M. Fox

; TITLE OF INVENTION: TNFr/OPG-LIKE MOLECULES AND USES THEREOF

; FILE REFERENCE: 01017/36854

; CURRENT APPLICATION NUMBER: US/10/146,574

; CURRENT FILING DATE: 2002-05-15

; PRIOR APPLICATION NUMBER: US/09/724,037

; PRIOR FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 27

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide

US-10-146-574-27

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4

|||

Db 3 KKK 5

RESULT 71

US-10-116-391-10

; Sequence 10, Application US/10116391

; Publication No. US20030087255A1

; GENERAL INFORMATION:

; APPLICANT: BARRITAULT, DENIS

; APPLICANT: ACHOUR, AMMAR

; APPLICANT: COURTY, JOSE

; TITLE OF INVENTION: PEPTIDES WHICH STIMULATE THE IMMUNE RESPONSE AND TISSUE

; TITLE OF INVENTION: REGENERATION

; FILE REFERENCE: 1081-02

; CURRENT APPLICATION NUMBER: US/10/116,391

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: PCT/FR00/02786

; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: FR 99/12714

; PRIOR FILING DATE: 1999-10-12

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: MK peptide fragment
US-10-116-391-10

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KKK 4
|||
Db 1 KKK 3

RESULT 72
US-10-139-084-4

; Sequence 4, Application US/10139084
; Publication No. US20030087313A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Dose Response-Based Methods For
; TITLE OF INVENTION: Identifying Receptors Having Alterations in Signaling
; FILE REFERENCE: 00398/515002
; CURRENT APPLICATION NUMBER: US/10/139,084
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/288,647
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-084-4

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQK 7
|||
Db 2 EQK 4

RESULT 73
US-10-075-869-26

; Sequence 26, Application US/10075869
; Publication No. US20030104622A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Mi, Zhibao
; APPLICANT: Frizzell, Raymond
; APPLICANT: Glorioso, Joseph C.
; APPLICANT: Gambotto, Andrea

; TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT
; TITLE OF INVENTION: FACILITATE UPTAKE AND CYTOPLASMIC AND/OR NUCLEAR
TRANSPORT
; TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES
; FILE REFERENCE: AP32573-AAA 072396.0237
; CURRENT APPLICATION NUMBER: US/10/075,869
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/151,980
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/188,944
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: random peptide library
US-10-075-869-26

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
 |||
Db 4 AKK 6

RESULT 74
US-10-109-171-113
; Sequence 113, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-10-109-171-113

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 9 AKK 11

RESULT 75
US-10-109-171-139
; Sequence 139, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 11
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: AMIDATION
US-10-109-171-139

Query Match 27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKK 3
|||
Db 8 AKK 10

Search completed: April 8, 2004, 16:35:49
Job time : 31.3077 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds
(without alignments)
124.984 Million cell updates/sec

Title: US-09-787-443A-20

Perfect score: 11

Sequence: 1 AKKKEQKQRNA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL_25:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rat:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				
No.	Score	Match	Length	DB	ID

Description

1	3	27.3	11	4	Q9H4H5	Q9h4h5 homo sapien
2	2	18.2	11	2	Q68237	Q68237 borrelia bu
3	2	18.2	11	2	Q9R790	Q9r790 borrelia ga
4	2	18.2	11	2	Q9L4F7	Q914f7 bacillus ce
5	2	18.2	11	2	Q47606	Q47606 escherichia
6	2	18.2	11	2	Q9S618	Q9s618 prochloroco
7	2	18.2	11	2	Q9S623	Q9s623 prochloroco
8	2	18.2	11	2	Q9EUZ3	Q9euz3 escherichia
9	2	18.2	11	2	Q47600	Q47600 escherichia
10	2	18.2	11	2	Q9RBV0	Q9rbv0 pseudomonas
11	2	18.2	11	2	Q9K332	Q9k332 staphylococ
12	2	18.2	11	2	Q9RFZ2	Q9rfz2 mycoplasma
13	2	18.2	11	2	P95518	P95518 pasteurella
14	2	18.2	11	2	Q47420	Q47420 escherichia
15	2	18.2	11	2	Q44090	Q44090 acholeplasm
16	2	18.2	11	2	Q56413	Q56413 escherichia
17	2	18.2	11	2	Q9R446	Q9r446 neisseria g
18	2	18.2	11	2	Q91UY9	Q91uy9 escherichia
19	2	18.2	11	2	Q8GMU3	Q8gmu3 acinetobact
20	2	18.2	11	2	Q47569	Q47569 escherichia
21	2	18.2	11	3	Q9UR95	Q9ur95 pichia angu
22	2	18.2	11	4	Q9UCP2	Q9ucp2 homo sapien
23	2	18.2	11	4	Q9Y3G2	Q9y3g2 homo sapien
24	2	18.2	11	4	Q60761	Q60761 homo sapien
25	2	18.2	11	4	Q9UC46	Q9uc46 homo sapien
26	2	18.2	11	5	Q26092	Q26092 pisaster oc
27	2	18.2	11	5	Q9Twx6	Q9twx6 manduca sex
28	2	18.2	11	5	Q25916	Q25916 plasmodium
29	2	18.2	11	5	Q9NFX0	Q9nfx0 drosophila
30	2	18.2	11	5	Q8MM58	Q8mm58 heliconius
31	2	18.2	11	5	Q86D32	Q86d32 trypanosoma
32	2	18.2	11	5	Q86D31	Q86d31 trypanosoma
33	2	18.2	11	5	Q95PX6	Q95px6 caenorhabdi
34	2	18.2	11	6	Q9TRW5	Q9trw5 bos taurus
35	2	18.2	11	6	P83128	P83128 bos indicus
36	2	18.2	11	7	Q7YP62	Q7yp62 homo sapien
37	2	18.2	11	8	Q8MEL7	Q8mel7 sida hooker
38	2	18.2	11	8	Q8MEM2	Q8mem2 lagunaria p
39	2	18.2	11	8	Q8MES5	Q8mes5 abelmoschus
40	2	18.2	11	8	Q8MEP0	Q8mep0 hibiscus pe
41	2	18.2	11	8	Q8MER8	Q8mer8 dombeya til
42	2	18.2	11	8	Q8MES1	Q8mes1 alyogyne pi
43	2	18.2	11	8	Q8MEP3	Q8mep3 hibiscus no
44	2	18.2	11	8	Q8MEQ7	Q8meq7 hibiscus dr
45	2	18.2	11	8	Q35374	Q35374 paramecium
46	2	18.2	11	8	Q8MEL9	Q8mel9 pavonia has
47	2	18.2	11	8	Q8MERO	Q8mer0 hibiscus co
48	2	18.2	11	8	Q8MES3	Q8mes3 alyogyne cr
49	2	18.2	11	8	Q8MEP5	Q8mep5 hibiscus mi
50	2	18.2	11	8	Q8MER1	Q8mer1 hibiscus ca
51	2	18.2	11	8	Q8MER7	Q8mer7 fioria viti
52	2	18.2	11	9	Q38415	Q38415 bacterioph
53	2	18.2	11	9	Q37925	Q37925 bacterioph
54	2	18.2	11	10	Q39784	Q39784 gossypium h
55	2	18.2	11	10	Q9T0L9	Q9t019 brassica ol
56	2	18.2	11	10	Q82070	Q82070 triticum ae
57	2	18.2	11	10	Q04131	Q04131 lycopersico

58	2	18.2	11	10	P82336	P82336 pisum sativ
59	2	18.2	11	11	Q9R0K9	Q9r0k9 mus musculu
60	2	18.2	11	12	P89269	P89269 xestia c-ni
61	2	18.2	11	12	Q69269	Q69269 equine herp
62	2	18.2	11	13	Q9PST1	Q9pst1 fugu rubrip
63	2	18.2	11	13	Q90735	Q90735 gallus gall
64	2	18.2	11	13	Q800X7	Q800x7 chelydra se
65	2	18.2	11	13	Q7T285	Q7t285 geochelone
66	2	18.2	11	13	Q7T284	Q7t284 geochelone
67	2	18.2	11	13	Q7T283	Q7t283 geochelone
68	2	18.2	11	13	Q7SX72	Q7sx72 geochelone
69	2	18.2	11	13	Q7SX71	Q7sx71 geochelone
70	2	18.2	11	15	Q83410	Q83410 mouse mamma
71	2	18.2	11	16	Q9K7A4	Q9k7a4 bacillus ha
72	1	9.1	11	2	Q9AIY6	Q9aiy6 carsonella
73	1	9.1	11	2	Q48933	Q48933 mycobacteri
74	1	9.1	11	2	Q47451	Q47451 escherichia
75	1	9.1	11	2	Q9AIZ7	Q9aiz7 carsonella
76	1	9.1	11	2	Q8RKN1	Q8rkn1 escherichia
77	1	9.1	11	2	Q52526	Q52526 rhizobium s
78	1	9.1	11	2	Q8KHL0	Q8kh10 streptococc
79	1	9.1	11	2	Q47602	Q47602 escherichia
80	1	9.1	11	2	Q9R4B1	Q9r4b1 streptococc
81	1	9.1	11	2	Q8L2T4	Q8l2t4 neisseria m
82	1	9.1	11	2	Q9R7U8	Q9r7u8 pseudomonas
83	1	9.1	11	2	Q9R5P3	Q9r5p3 serratia ma
84	1	9.1	11	2	P77404	P77404 escherichia
85	1	9.1	11	2	Q9RQ60	Q9rq60 buchnera ap
86	1	9.1	11	2	P96319	P96319 desulfovibr
87	1	9.1	11	2	Q93RM6	Q93rm6 staphylococ
88	1	9.1	11	2	Q8RMI8	Q8rmi8 enterococcu
89	1	9.1	11	2	Q87882	Q87882 mycobacteri
90	1	9.1	11	2	Q8KTN1	Q8ktn1 candidatus
91	1	9.1	11	2	P71228	P71228 escherichia
92	1	9.1	11	2	Q93MI7	Q93mi7 escherichia
93	1	9.1	11	2	Q47604	Q47604 escherichia
94	1	9.1	11	2	Q47345	Q47345 escherichia
95	1	9.1	11	2	Q9AIZ8	Q9aiz8 carsonella
96	1	9.1	11	2	Q8KRA1	Q8kra1 streptococc
97	1	9.1	11	2	Q47059	Q47059 escherichia
98	1	9.1	11	2	Q44237	Q44237 anabaena sp
99	1	9.1	11	2	Q9R872	Q9r872 escherichia
100	1	9.1	11	2	Q56972	Q56972 yersinia pe

ALIGNMENTS

RESULT 1

Q9H4H5

ID Q9H4H5 PRELIMINARY; PRT; 11 AA.
 AC Q9H4H5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE DJ661I20.2 (Novel helicase C-terminal domain and SNF2 N-terminal
 DE domains containing protein) (Fragment).

GN DJ620E11.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Skuce C.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL031669; CAC17164.2; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1420 MW; 5EB2C32A3326D053 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKE 5
|||
Db 7 KKE 9

RESULT 2
068237
ID 068237 PRELIMINARY; PRT; 11 AA.
AC 068237;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Plasmid cp32-4, possible partition proteins (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-4.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RT Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022481; AAC35449.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1237 MW; 50E3B714D45B5DD7 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
|||
Db 7 NA 8

RESULT 3

Q9R790

ID Q9R790 PRELIMINARY; PRT; 11 AA.
 AC Q9R790;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Outer surface protein C (Fragment).
 GN OSPC.
 OS *Borrelia garinii*.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.
 OX NCBI_TaxID=29519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G25;
 RX MEDLINE=97426044; PubMed=9282748;
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "he *Borrelia burgdorferi* circular plasmid cp26: conservation of
 plasmid structure and targeted inactivation of the *ospC* gene.";
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL; U93700; AAC45535.1; -.
 DR GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.
 DR GO:0003793; F:defense/immunity protein activity; IEA.
 DR GO:0006952; P:defense response; IEA.
 DR InterPro; IPR001800; Lipoprotein_6.
 DR Pfam; PF01441; Lipoprotein_6; 1.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
 ||
 Db 2 KK 3

RESULT 4

Q9L4F7

ID Q9L4F7 PRELIMINARY; PRT; 11 AA.
 AC Q9L4F7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Phosphatidylinositol-specific phospholipase C (PI-PLC)
 DE (Fragment).
 GN PLCA.
 OS *Bacillus cereus*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14579 type strain;
 RX MEDLINE=20055637; PubMed=10589720;

RA Okstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;
RT "Sequence analysis of three *Bacillus cereus* loci under PICR-regulated
RT genes encoding degradative enzymes and enterotoxin.";
RL *Microbiology* 145:3129-3138 (1999).
DR EMBL; AJ243711; CAB69804.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 4 KK 5

RESULT 5

Q47606

ID Q47606 PRELIMINARY; PRT; 11 AA.
AC Q47606;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE REase protein (Fragment).
GN REASE.
OS *Escherichia coli*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Escherichia*.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL *J. Bacteriol.* 173:1367-1375 (1991).
DR EMBL; M63622; AAA24562.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 5 KE 6

RESULT 6

Q9S618

ID Q9S618 PRELIMINARY; PRT; 11 AA.
AC Q9S618;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE Cytochrome b6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070132; AAD20740.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 5 KK 6

RESULT 7
Q9S623
ID Q9S623 PRELIMINARY; PRT; 11 AA.
AC Q9S623;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b (Fragment).
GN PETB.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070168; AAD23221.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1153 MW; 5F551A5CB05866D3 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 4 KQ 5

RESULT 8

Q9EUZ3

ID Q9EUZ3 PRELIMINARY; PRT; 11 AA.
 AC Q9EUZ3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Ribosome binding factor A (Fragment).
 GN RBFA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IQ490;
 RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
 RA Mortensen K.K.;
 RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
 RT IQ490.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ132862; CAC20133.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 2 AK 3

RESULT 9

Q47600

ID Q47600 PRELIMINARY; PRT; 11 AA.
 AC Q47600;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE REase protein (Fragment).
 GN REASE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 RT modification systems.";
 RL J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63619; AAA24556.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1232 MW; 63175479572AB5A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 9 NA 10

RESULT 10

Q9RBV0

ID Q9RBV0 PRELIMINARY; PRT; 11 AA.
AC Q9RBV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Resolvase (Fragment).
OS Pseudomonas sp. R9.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=101164;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R9; TRANSPOSON=Tn1404;
RX MEDLINE=20011227; PubMed=10543801;
RA Schnabel E.L., Jones A.L.;
RT "Distribution of tetracycline resistance genes and transposons among
RT phylloplane bacteria in Michigan apple orchards.";
RL Appl. Environ. Microbiol. 65:4898-4907(1999).
DR EMBL; AF157800; AAD48002.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1307 MW; D00B18E258704416 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QR 9
||
Db 4 QR 5

RESULT 11

Q9K332

ID Q9K332 PRELIMINARY; PRT; 11 AA.
AC Q9K332;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Geh (Fragment).
GN GEH.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=VARIOUS STRAINS;
RX MEDLINE=20187516; PubMed=10722640;
RA Cramton S.E., Schnell N.F., Gotz F., Bruckner R.;
RT "Identification of a new repetitive element in *Staphylococcus*
RT *aureus*.";
RL Infect. Immun. 68:2344-2348 (2000).
DR EMBL; AF195967; AAF60251.1; -.
DR EMBL; AF195963; AAF60243.1; -.
DR EMBL; AF195964; AAF60245.1; -.
DR EMBL; AF195965; AAF60247.1; -.
DR EMBL; AF195966; AAF60249.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1262 MW; 4F978F86AAB1A723 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 9 KQ 10

RESULT 12
Q9RFZ2
ID Q9RFZ2 PRELIMINARY; PRT; 11 AA.
AC Q9RFZ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fructose biphosphate aldolase (Fragment).
GN FBA.
OS Mycoplasma mycoides subsp. capri.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=40477;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG3;
RX MEDLINE=20193983; PubMed=10727835;
RA Thiaucourt F., Lorenzon S., David A., Breard A.;
RT "Phylogeny of the *Mycoplasma mycoides* cluster as shown by sequencing
RT of a putative membrane protein gene.";
RL Vet. Microbiol. 72:251-268 (2000).
DR EMBL; AF162998; AAF15255.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1371 MW; 50B0881A3331FB57 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 7 KK 8

RESULT 13

P95518

ID P95518 PRELIMINARY; PRT; 11 AA.
AC P95518;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein RpsA (Fragment).
GN RPSA.
OS Pasteurella haemolytica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHL101;
RX MEDLINE=97164347; PubMed=9011038;
RA Highlander S.K., Garza O., Brown B.J., Koby S., Oppenheim A.B.;
RT "Isolation and characterization of the integration host factor genes
RT of Pasteurella haemolytica.";
RL FEMS Microbiol. Lett. 146:181-188(1997).
DR EMBL; U56139; AAC44845.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1168 MW; 7A4BFD38D339CDDDB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 8 AK 9

RESULT 14

Q47420
ID Q47420 PRELIMINARY; PRT; 11 AA.
AC Q47420;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF11 protein.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92041688; PubMed=1657895;
RA Sharples G.J., Lloyd R.G.;
RT "Resolution of Holliday junctions in Escherichia coli: Identification
RT of the ruvC gene product as a 19-Kilodalton protein.";
RL J. Bacteriol. 173:7711-7715(1991).
DR EMBL; X59551; CAA42127.1; -.
DR PIR; S19015; S19015.
SQ SEQUENCE 11 AA; 1215 MW; DD8D6D4D56C6D33D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 4 AK 5

RESULT 15

Q44090

ID Q44090 PRELIMINARY; PRT; 11 AA.
AC Q44090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical export segment (Fragment).
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A-EF22;
RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;
RT "Sequence regions from Acholeplasma laidlawii which restore export of
RT beta-lactamase in Escherichia coli.";
RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z22875; CAA80495.1; -.
DR PIR; S33519; S33519.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 2 KK 3

RESULT 16

Q56413

ID Q56413 PRELIMINARY; PRT; 11 AA.
AC Q56413;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IS602L region DNA, 5' end (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Transposon Tn602;

RX MEDLINE=87318208; PubMed=2819910;
RA Stibitz S., Davies J.E.;
RT "Tn602: A naturally occurring relative of Tn903 with direct repeats.";
RL Plasmid 17:202-209(1987).
DR EMBL; M22735; AAA27464.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1361 MW; 447E8354A05339C3 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 17
Q9R446
ID Q9R446 PRELIMINARY; PRT; 11 AA.
AC Q9R446;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Carbamoyl-phosphate synthase subunit A (Fragment).
GN CARA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RX MEDLINE=95291461; PubMed=7773412;
RA Lawson F.S., Billowes F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
gonorrhoeae includes a large, variable intergenic sequence which is
also present in other Neisseria species.";
RL Microbiology 141:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
synthase genes of Neisseria species.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF029363; AAC78453.1; -.
DR EMBL; AF029362; AAC78452.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DDD33694 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AK 2

||
Db 8 AK 9

RESULT 18
Q91UY9
ID Q91UY9 PRELIMINARY; PRT; 11 AA.
AC Q91UY9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Insertion site for insertion element IS903.B, upstream of kanamycin
DE resistance gene (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPONSON=Tn2680;
RX MEDLINE=85234397; PubMed=2989253;
RA Mollet B., Clerget M., Meyer J., Iida S.;
RT "Organization of the Tn6-related kanamycin resistance transposon
RT Tn2680 carrying two copies of IS26 and an IS903 variant, IS903.B.";
RL J. Bacteriol. 163:55-60(1985).
DR EMBL; M11420; AAA27427.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1278 MW; 03902598AB0416D0 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QR 9
||
Db 5 QR 6

RESULT 19
Q8GMU3
ID Q8GMU3 PRELIMINARY; PRT; 11 AA.
AC Q8GMU3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative catalase isozyme (Fragment).
GN KATA.
OS Acinetobacter lwoffii.
OG Plasmid pKLH202.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=28090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TC108;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;

RT "pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ250245; CAC80800.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1233 MW; 81A15757B333276A CRC64;
Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 6 KK 7

RESULT 20
Q47569
ID Q47569 PRELIMINARY; PRT; 11 AA.
AC Q47569;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=94162733; PubMed=7764507;
RA Yamada M., Yanai S., Talkuder A.;
RT "Analysis of products of the Escherichia coli genomic genes and
RT regulation of their expressions: an applicable procedure for genomic
RT analysis of other microorganisms.";
RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
DR EMBL; D21156; BAA04692.1; -.
KW Hypothetical protein.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1322 MW; C0B8E40E37672732 CRC64;
Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 9 KQ 10

RESULT 21
Q9UR95
ID Q9UR95 PRELIMINARY; PRT; 11 AA.
AC Q9UR95;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Heat shock protein 60 homolog (Fragment).
OS *Pichia angusta* (Yeast) (*Hansenula polymorpha*).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; *Pichia*.
OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE.
RX MEDLINE=93223840; PubMed=8096822;
RA Evers M.E., Huhse B., Titorenko V.I., Kunau W.H., Hartl F.U.,
RA Harder W., Veenhuis M.;
RT "Affinity purification of molecular chaperones of the yeast *Hansenula*
RT *polymorpha* using immobilized denatured alcohol oxidase.";
RL FEBS Lett. 321:32-36(1993).
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 3 KE 4

RESULT 22
Q9UCP2
ID Q9UCP2 PRELIMINARY; PRT; 11 AA.
AC Q9UCP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE cGMP-inhibited LOW K(M) cAMP phosphodiesterase PEAK 43, CGI-PDE
DE (Fragment).
OS *Homo sapiens* (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; *Homo*.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92283180; PubMed=1317779;
RA LeBon T.R., Kasuya J., Paxton R.J., Belfrage P., Hockman S.,
RA Manganiello V.C., Fujita Yamaguchi Y.;
RT "Purification and characterization of guanosine 3',5'-monophosphate-
RT inhibited low K(m) adenosine 3',5'-monophosphate phosphodiesterase
RT from human placental cytosolic fractions.";
RL Endocrinology 130:3265-3274(1992).
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1220 MW; 7DF1FDF2D44735BB CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 7 NA 8

RESULT 23

Q9Y3G2

ID Q9Y3G2 PRELIMINARY; PRT; 11 AA.
AC Q9Y3G2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE LSFR2 protein (Fragment).
GN LSFR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99299247; PubMed=10369878;
RA Gilley J., Fried M.;
RT "Extensive gene order differences within regions of conserved synteny
RT between the Fugu and human genomes: implications for chromosomal
RT evolution and the cloning of disease genes.";
RL Hum. Mol. Genet. 8:1313-1320(1999).
DR EMBL; Y17456; CAB44349.1; --.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1342 MW; 68C5E5D7A8772324 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QR 9
||
Db 3 QR 4

RESULT 24

O60761

ID O60761 PRELIMINARY; PRT; 11 AA.
AC O60761;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NPT-1 protein (Fragment).
GN NPT-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=98207718; PubMed=9545579;
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,
RA Tatsumi S., Morita K., Takeda E.;
RT "Characterization of the 5' flanking region of the human NPT-1
RT Na+/phosphate cotransporter gene.";
RL Biochim. Biophys. Acta 1396:267-272(1998).
DR EMBL; D83236; BAA25645.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 10 KK 11

RESULT 25
Q9UC46
ID Q9UC46 PRELIMINARY; PRT; 11 AA.
AC Q9UC46;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neutrophil inhibitor peptide, NIP=POLYMORPHONUCLEAR neutrophil
DE inhibitor peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=96326114; PubMed=8703476;
RA Cooper J.A.Jr., Culbreth R.R.;
RT "Characterization of a neutrophil inhibitor peptide harvested from
RT human bronchial lavage: homology to influenza A nucleoprotein.";
RL Am. J. Respir. Cell Mol. Biol. 15:207-215(1996).
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0030236; P:anti-inflammatory response; NAS.
SQ SEQUENCE 11 AA; 1262 MW; 951A1C3279C9DB45 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 10 NA 11

RESULT 26
Q26092
ID Q26092 PRELIMINARY; PRT; 11 AA.
AC Q26092;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Sea STAR histone H2B gene 5'region (Fragment).
OS Pisaster ochraceus (Sea star).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Pisaster.
OX NCBI_TaxID=7612;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sperm;
RA Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;
RT "Organization and Unusual Expression of Histone Genes in the Sea Star
RT Pisaster ochraceus.";
RL J. Mol. Evol. 25:29-36(1987).
DR EMBL; X05619; CAA29106.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QK 7
||
Db 10 QK 11

RESULT 27
Q9TWX6
ID Q9TWX6 PRELIMINARY; PRT; 11 AA.
AC Q9TWX6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide
DE (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=92134256; PubMed=1734862;
RA Touhara K., Prestwich G.D.;
RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
RT binding protein.";
RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 10 AK 11

RESULT 28

Q25916
ID Q25916 PRELIMINARY; PRT; 11 AA.
AC Q25916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Malaria antigen (7H8/2) (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91164876; PubMed=1706114;
RA Limpaiboon T., Taylor D., Jones G., Geysen H.M., Saul A.;
RT "Characterization of a Plasmodium falciparum epitope recognized by a
monoclonal antibody with broad isolate and species specificity.";
RL Southeast Asian J. Trop. Med. Public Health 21:388-396(1990).
DR EMBL; M31305; AAA29645.1; -.
FT NON TER 1 1
SQ SEQUENCE 11 AA; 1415 MW; DB03D3BC42C33699 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10
||
Db 9 RN 10

RESULT 29

Q9NFX0
ID Q9NFX0 PRELIMINARY; PRT; 11 AA.
AC Q9NFX0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mitochondrial aconitase (Fragment).
GN ACON OR MAC OR CG9244.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriodea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S;
RA Lind M.I.;
RT "Charaterisation of two iron regulatory proteins and mitochondrial
aconitase in Drosophila melanogaster.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ252019; CAB93522.1; -.
DR FlyBase; FBgn0010100; Acon.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1204 MW; 7C889CE4D4469734 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 7 NA 8

RESULT 30

Q8MM58

ID Q8MM58 PRELIMINARY; PRT; 11 AA.
AC Q8MM58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN MPI.
OS Heliconius cydno chioneus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilioidea; Nymphalidae; Heliconiinae; Heliconius.
OX NCBI_TaxID=171915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRI-B-553-Mpi-1, and STRI-B-553-Mpi-2;
RA Bull V., Beltran M., Birmingham E., Jiggins C., McMillan O.,
RA Mallet J.;
RT "Molecular evidence for gene flow between species of Heliconius.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF516222; AAM61908.1; -.
DR EMBL; AF516223; AAM61909.1; -.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1312 MW; 56A67DB31DD1EAA3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||
Db 8 EQ 9

RESULT 31

Q86D32

ID Q86D32 PRELIMINARY; PRT; 11 AA.
AC Q86D32;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histone H1 (Fragment).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dm28c;
RX MEDLINE=22557728; PubMed=12670512;
RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
RA Campbell D.A.;
RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";
RL Int. J. Parasitol. 33:269-279(2003).
DR EMBL; AF545075; AAP21903.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1114 MW; CCC1B31E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 9 KK 10

RESULT 32
Q86D31
ID Q86D31 PRELIMINARY; PRT; 11 AA.
AC Q86D31;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histone H1 (Fragment).
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sylvio X10;
RX MEDLINE=22557728; PubMed=12670512;
RA Sturm N.R., Vargas N.S., Westenberger S.J., Zingales B.,
RA Campbell D.A.;
RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";
RL Int. J. Parasitol. 33:269-279(2003).
DR EMBL; AF545076; AAP21906.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1174 MW; CCD1B21E7772CDDD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 9 KK 10

RESULT 33

Q95PX6

ID Q95PX6 PRELIMINARY; PRT; 11 AA.
AC Q95PX6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ZK1236.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Favello A.;
RT "The sequence of C. elegans cosmid ZK1236.";
RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; L13200; AAL11108.1; --.
DR WormPep; ZK1236.8; CE29629.
KW Hypothetical protein.
SQ SEQUENCE 11 AA; 1304 MW; DFA3510A25A76322 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 8 KK 9

RESULT 34

Q9TRW5

ID Q9TRW5 PRELIMINARY; PRT; 11 AA.
AC Q9TRW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 25 kDa protein P25, peptide F4 (Fragment).

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
RL FEBS Lett. 289:37-43(1991).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 1 KE 2

RESULT 35
P83128
ID P83128 PRELIMINARY; PRT; 11 AA.
AC P83128;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pregnancy-associated glycoprotein (Fragment).
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9915;
RN [1]
RP SEQUENCE, AND GLYCOSYLATION.
RC TISSUE=Placenta;
RA Sousa N.M., Remy B., El Amiri B., Figueiredo J.R., Beckers J.F.;
RT "Characterization of pregnancy-associated glycoproteins extracted from
RT zebu (Bos indicus) placentas removed at different gestational
RT periods.";
RL Submitted (OCT-2001) to Swiss-Prot.
CC -!- PTM: GLYCOSYLATED.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; NAS.
DR GO; GO:0016787; F:hydrolase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
KW Glycoprotein.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1234 MW; CE8EA47EA0586B5D CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 3 NA 4

RESULT 36

Q7YP62

ID Q7YP62 PRELIMINARY; PRT; 11 AA.
AC Q7YP62;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class Ib antigen (Fragment).
GN HLA-F.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., He X., Xu L., Zeng Y.;
RT "Partial genomic sequence of HLA-F gene.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY328516; AAP94210.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1208 MW; 2E0B6C5CC5AB45B8 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10
||
Db 1 RN 2

RESULT 37

Q8MEL7

ID Q8MEL7 PRELIMINARY; PRT; 11 AA.
AC Q8MEL7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Sida hookeriana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Sida.
OX NCBI_TaxID=108446;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using

RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";
RL *Syst. Bot.* 27:333-350(2002).
DR EMBL; AF384624; AAM50396.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 38
Q8MEM2
ID Q8MEM2 PRELIMINARY; PRT; 11 AA.
AC Q8MEM2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS *Lagunaria patersonia*.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; *Lagunaria*.
OX NCBI_TaxID=183274;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of *Hibiscus* and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";
RL *Syst. Bot.* 27:333-350(2002).
DR EMBL; AF384616; AAM50388.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 39
Q8MES5

ID Q8MES5 PRELIMINARY; PRT; 11 AA.
AC Q8MES5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Abelmoschus manihot.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.
OX NCBI_TaxID=183220;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384561; AAM50399.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 40
Q8MEP0
ID Q8MEP0 PRELIMINARY; PRT; 11 AA.
AC Q8MEP0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus peralbus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183256;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384598; AAM50370.1; -

DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 41
Q8MER8
ID Q8MER8 PRELIMINARY; PRT; 11 AA.
AC Q8MER8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Dombeya tiliacea.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Dombeyoideae; Dombeya.
OX NCBI_TaxID=121875;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384569; AAM50407.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1424 MW; 7227C351D32AE9D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 42
Q8MES1
ID Q8MES1 PRELIMINARY; PRT; 11 AA.
AC Q8MES1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Alyogyne pinoniana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
OX NCBI_TaxID=183226;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384566; AAM50404.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;
Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 43
Q8MEP3
ID Q8MEP3 PRELIMINARY; PRT; 11 AA.
AC Q8MEP3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus normanii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183253;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384595; AAM50367.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;
Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 44

Q8MEQ7
ID Q8MEQ7 PRELIMINARY; PRT; 11 AA.
AC Q8MEQ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus drummondii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183239;

RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384581; AAM50353.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.

FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 45

Q35374
ID Q35374 PRELIMINARY; PRT; 11 AA.
AC Q35374;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P1 protein (Fragment).

OS Paramecium tetraurelia.
 OG Mitochondrion.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 OC Paramecium.
 OX NCBI_TaxID=5888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=stock 172;
 RX MEDLINE=87055241; PubMed=3023187;
 RA Pritchard A.E., Seilhamer J.J., Cummings D.J.;
 RT "Paramecium mitochondrial DNA sequences and RNA transcripts for
 cytochrome oxidase subunit I, URF1, and three ORFs adjacent to the
 replication origin.";
 RL Gene 44:243-253(1986).
 DR EMBL; M15280; AAA79267.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1266 MW; 1D84259D16D046D4 CRC64;

 Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 8 QR 9
 ||
 Db 7 QR 8

RESULT 46
 Q8MEL9
 ID Q8MEL9 PRELIMINARY; PRT; 11 AA.
 AC Q8MEL9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Pavonia hastata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Pavonia.
 OX NCBI_TaxID=183278;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384622; AAM50394.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 47

Q8MERO

ID Q8MERO PRELIMINARY; PRT; 11 AA.
AC Q8MERO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus coatesii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183236;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384578; AAM50416.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 48

Q8MES3

ID Q8MES3 PRELIMINARY; PRT; 11 AA.
AC Q8MES3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Alyogyne cravenii.
OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Alyogyne.
OX NCBI_TaxID=183223;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384563; AAM50401.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 49
Q8MEP5
ID Q8MEP5 PRELIMINARY; PRT; 11 AA.
AC Q8MEP5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus microchlaenus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183251;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384593; AAM50365.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 50

Q8MER1

ID Q8MER1 PRELIMINARY; PRT; 11 AA.
AC Q8MER1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Hibiscus calyphyllus.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
OX NCBI_TaxID=183235;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384577; AAM50415.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 51

Q8MER7

ID Q8MER7 PRELIMINARY; PRT; 11 AA.
AC Q8MER7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Fioria vitifolia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Fioria.

OX NCBI_TaxID=183231;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
chloroplast DNA sequences of *ndhF* and the *rpl16* intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384570; AAM50408.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KQ 8
||
Db 7 KQ 8

RESULT 52
Q38415
ID Q38415 PRELIMINARY; PRT; 11 AA.
AC Q38415;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ant1 protein (Fragment).
OS Bacteriophage P7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P1-like viruses.
OX NCBI_TaxID=10682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90335968; PubMed=1696181;
RA Citron M., Schuster H.;
RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";
RL Cell 62:591-598(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92319637; PubMed=1620606;
RA Citron M., Schuster H.;
RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense
RNA.";
RL Nucleic Acids Res. 20:3085-3090(1992).
DR EMBL; M35139; AAA32437.1; -.
DR PIR; S42449; S42449.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1315 MW; 38A55C6D11B2C737 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 2 KK 3

RESULT 53

Q37925

ID Q37925 PRELIMINARY; PRT; 11 AA.
AC Q37925;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Bacteriophage fr replicase (Fragment).
OS Bacteriophage fr.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus.
OX NCBI_TaxID=12017;
RN [1]
RP SEQUENCE FROM N.A.
RA Berzin V.M., Gribanov V.A., Cielens I.E., Jansone I.V., Gren E.J.;
RT "The nucleotide sequence of the regulatory region of phage fr
replicase cistron.";
RL Bioorg. Khim. 7:306-308(1981).
DR EMBL; M34834; AAA32193.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1285 MW; 8BD43470C33321B1 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 6 KK 7

RESULT 54

Q39784

ID Q39784 PRELIMINARY; PRT; 11 AA.
AC Q39784;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE Alcohol dehydrogenase 2b-2 (Fragment).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Blue Tag Siokra;
RA Millar A.A., Dennis E.S.;
RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U53705; AAA98988.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1161 MW; D67F443942D6D87D CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 10 AK 11

RESULT 55

Q9T0L9

ID Q9T0L9 PRELIMINARY; PRT; 11 AA.
AC Q9T0L9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SLG5 protein (Fragment).
GN SLG5.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99264316; PubMed=10330480;
RA Cabrillac D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
RA Dumas C., Gaude T., Cock J.M.;
RT "The S15 self-incompatibility haplotype in Brassica includes three S
RT gene family members which are expressed in stigmas.";
RL Plant Cell 11:971-986(1999).
DR EMBL; Y18256; CAB41875.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1035 MW; CD3806DDA8772AAD CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 2 NA 3

RESULT 56

O82070

ID O82070 PRELIMINARY; PRT; 11 AA.
AC O82070;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RNA polymerase (EC 2.7.7.6) (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.

OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Chinese Spring;
 RA Young D.A., Allen R., Harvey A.J., Lonsdale D.M.;
 RT "Characterization of a gene encoding a single-subunit RNA polymerase
 from maize which is alternatively spliced.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ005344; CAA06489.1; -.
 DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0003900; F:DNA-directed RNA polymerase I activity; IEA.
 DR GO; GO:0003901; F:DNA-directed RNA polymerase II activity; IEA.
 DR GO; GO:0003902; F:DNA-directed RNA polymerase III activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Nucleotidyltransferase; Transferase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1329 MW; CD96344923240AB2 CRC64;

 Query Match 18.2%; Score 2; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 KQ 8
 ||
 Db 10 KQ 11

 RESULT 57
 Q04131
 ID Q04131 PRELIMINARY; PRT; 11 AA.
 AC Q04131;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Wound induced protein (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=pik-red; TISSUE=Pericarp;
 RX MEDLINE=91355936; PubMed=1715787;
 RA Parsons B.L., Mattoo A.K.;
 RT "Wound regulated accumulation of specific transcripts in tomato fruit:
 interactions with fruit development, ethylene and light.";
 RL Plant Mol. Biol. 17:453-464(1991).
 DR EMBL; X59884; CAA42539.1; -.
 DR PIR; S19775; S19775.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1278 MW; 92CB257828733325 CRC64;

 Query Match 18.2%; Score 2; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KK 3
||
Db 5 KK 6

RESULT 58

P82336

ID P82336 PRELIMINARY; PRT; 11 AA.
AC P82336;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT125) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.8, ITS MW IS: 45.8 KDA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0009579; C:thylakoid; IEA.
KW Chloroplast; Thylakoid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1255 MW; 13511E6EDB1DDB10 CRC64;

Query Match 18.2%; Score 2; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||
Db 7 EQ 8

RESULT 59

Q9R0K9

ID Q9R0K9 PRELIMINARY; PRT; 11 AA.
AC Q9R0K9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bcl-2 associated X protein (Fragment).
GN BAX.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20035745; PubMed=10570968;
 RA Igata E., Inoue T., Ohtani-Fujita N., Sowa Y., Tsujimoto Y., Sakai T.;
 RT "Molecular cloning and functional analysis of the murine bax gene
 promoter.";
 RL Gene 238:407-415(1999).
 DR EMBL; AB029557; BAA82406.1; -.
 DR MGD; MGI:99702; Bax.
 DR GO; GO:0016506; F:apoptosis activator activity; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0006915; P:apoptosis; IDA.
 DR GO; GO:0008635; P:caspase activation via cytochrome c; IDA.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1037 MW; 90AAB34E36DB1865 CRC64;

 Query Match 18.2%; Score 2; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 5 EQ 6
 ||
 Db 6 EQ 7

RESULT 60
 P89269
 ID P89269 PRELIMINARY; PRT; 11 AA.
 AC P89269;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DNA binding protein homolog (Fragment).
 OS Xestia c-nigrum granulosis virus (XnGV) (Xestia c-nigrum
 OS granulovirus).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OX NCBI_TaxID=51677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=alpha-4;
 RX MEDLINE=98271593; PubMed=9608666;
 RA Goto C., Hayakawa T., Maeda S.;
 RT "Genome organization of Xestia c-nigrum granulovirus.";
 RL Virus Genes 16:199-210(1998).
 DR EMBL; U70897; AAB46487.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1371 MW; 6F05444F52C1E454 CRC64;

 Query Match 18.2%; Score 2; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 8 QR 9

||
Db 2 QR 3

RESULT 61
Q69269
ID Q69269 PRELIMINARY; PRT; 11 AA.
AC Q69269;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN IE.
OS Equine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10326;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kentucky A;
RX MEDLINE=90064773; PubMed=2555546;
RA Harty R.N., Colle C.F., Grundy F.J., O'Callaghan D.J.;
RT "Mapping the termini and intron of the spliced immediate-early
RT transcript of equine herpesvirus 1.";
RL J. Virol. 63:5101-5110(1989).
DR EMBL; M30497; AAA66553.1; -.
KW Hypothetical protein.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1224 MW; D93837E0CAB5A416 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QR 9
||
Db 4 QR 5

RESULT 62
Q9PST1
ID Q9PST1 PRELIMINARY; PRT; 11 AA.
AC Q9PST1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetradontoidea; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353;

RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80917.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1085 MW; D34649C3C2C735A2 CRC64;
Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 9 NA 10

RESULT 63
Q90735
ID Q90735 PRELIMINARY; PRT; 11 AA.
AC Q90735;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-globin gene (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81208060; PubMed=6263308;
RA Day L.E., Hirst A.J., Lai E.C., Mace M.Jr., Woo S.L.C.;
RT "5' domain and nucleotide sequence of an adult chicken chromosomal
RT beta-globin gene.";
RL Biochemistry 20:2091-2098(1981).
DR EMBL; V00378; CAA23677.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1372 MW; 271C02021B1DC1B3 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 KQ 8
||
Db 9 KQ 10

RESULT 64
Q800X7
ID Q800X7 PRELIMINARY; PRT; 11 AA.
AC Q800X7;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Vacuolar H-ATPase B subunit (Fragment).
 OS Chelydra serpentina serpentina (common snapping turtle).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
 OX NCBI_TaxID=134619;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21876906; PubMed=11882478;
 RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
 RT "Octylphenol (OP) alters the expression of members of the amyloid
 protein family in the hypothalamus of the snapping turtle, Chelydra
 serpentina serpentina.";
 RL Environ. Health Perspect. 110:269-275 (2002).
 DR EMBL; AF469184; AAO48730.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1350 MW; 2FC8B6D0B5BAB417 CRC64;

 Query Match 18.2%; Score 2; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 AK 2
 ||
 Db 9 AK 10

RESULT 65
 Q7T285
 ID Q7T285 PRELIMINARY; PRT; 11 AA.
 AC Q7T285;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Creatine kinase (Fragment).
 OS Geochelone carbonaria (Red-footed tortoise).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
 OX NCBI_TaxID=50047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=red;
 RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccone A.;
 RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
 the Giant Galapagos Tortoise.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY101746; AAM34549.1; -.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

 Query Match 18.2%; Score 2; DB 13; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 10 KE 11

RESULT 66
Q7T284
ID Q7T284 PRELIMINARY; PRT; 11 AA.
AC Q7T284;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone denticulata (Yellow footed tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=101697;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=yellow2;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccone A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY101747; AAM34550.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;
Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 10 KE 11

RESULT 67
Q7T283
ID Q7T283 PRELIMINARY; PRT; 11 AA.
AC Q7T283;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone pardalis (Leopard tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=55540;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=to;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccone A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in

RT the Giant Galapagos Tortoise.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY101748; AAM34551.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;
Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 10 KE 11

RESULT 68
Q7SX72
ID Q7SX72 PRELIMINARY; PRT; 11 AA.
AC Q7SX72;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone chilensis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=106216;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1864, and 8136;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccione A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY101744; AAM34547.1; -.
DR EMBL; AY101745; AAM34548.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;
Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 KE 5
||
Db 10 KE 11

RESULT 69
Q7SX71
ID Q7SX71 PRELIMINARY; PRT; 11 AA.
AC Q7SX71;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Creatine kinase (Fragment).
OS Geochelone nigra (Galapagos giant tortoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Testudinidae; Geochelone.
OX NCBI_TaxID=66189;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AG01, CAZ22, CRU1, ESP1, LG, ME4, PB3, P244, PZ6, and VA935;
RA Gentile G., Burns C., Sezzi E., Bergman W., Powell J.R., Caccone A.;
RT "Contrasting Patterns of Nuclear and Mitochondrial DNA Variation in
RT the Giant Galapagos Tortoise.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY101734; AAM34537.1; -.
DR EMBL; AY101735; AAM34538.1; -.
DR EMBL; AY101736; AAM34539.1; -.
DR EMBL; AY101737; AAM34540.1; -.
DR EMBL; AY101738; AAM34541.1; -.
DR EMBL; AY101739; AAM34542.1; -.
DR EMBL; AY101740; AAM34543.1; -.
DR EMBL; AY101741; AAM34544.1; -.
DR EMBL; AY101742; AAM34545.1; -.
DR EMBL; AY101743; AAM34546.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1356 MW; 6454ABA6733EB9D4 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 10 KE 11

RESULT 70
Q83410
ID Q83410 PRELIMINARY; PRT; 11 AA.
AC Q83410;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Superantigen (Fragment).
GN SAG.
OS Mouse mammary tumor virus.
OC Viruses; Retroviridae; Betaretrovirus.
OX NCBI_TaxID=11757;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mtv-6;
RX MEDLINE=95133174; PubMed=7831795;
RA Cho K., Ferrick D.A., Morris D.W.;
RT "Structure and biological activity of the subgenomic Mtv-6 endogenous
RT provirus.";

RL Virology 206:395-402(1995).
DR EMBL; L37518; AAA66963.1; -.
DR InterPro; IPR001213; MMTV_SAg.
DR Pfam; PF01054; MMTV_SAg; 1.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1401 MW; 5E6B080A7326C6D7 CRC64;

Query Match 18.2%; Score 2; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QK 7
||
Db 6 QK 7

RESULT 71
Q9K7A4
ID Q9K7A4 PRELIMINARY; PRT; 11 AA.
AC Q9K7A4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein BH3464.
GN BH3464.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001518; BAB07183.1; -.
DR PIR; H84082; H84082.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 11 AA; 1219 MW; 5F7D235CB7272B13 CRC64;

Query Match 18.2%; Score 2; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KE 5
||
Db 4 KE 5

RESULT 72
Q9AIY6
ID Q9AIY6 PRELIMINARY; PRT; 11 AA.
AC Q9AIY6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
RA Baumann P.;
RT "Cospeciation of psyllids and their primary prokaryotic
endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861 (2001).
DR EMBL; AF211138; AAK15388.1; -.
DR GO; GO:0004812; F:tRNA ligase activity; IEA.
KW Aminoacyl-tRNA synthetase.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1295 MW; 0CA993A5345B5720 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 8 K 8

RESULT 73

Q48933

ID Q48933 PRELIMINARY; PRT; 11 AA.
AC Q48933; P77701; Q48932;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Alkyl hydroperoxide reductase C (Fragment).
GN AHPC.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC35728, and ATCC35727;
RA Zhang Y., Deretic V.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC35735;

RX MEDLINE=96256622; PubMed=8655566;
RA Dhandayuthapani S., Zhang Y., Deretic V.;
RT "Oxidative stress response and its role in sensitivity to isoniazid in
RT mycobacteria: characterization and inducibility of ahpC by peroxides in
RT Mycobacterium smegmatis and lack of expression in M. aurum and M.
RT tuberculosis.";
RL J. Bacteriol. 178:3641-3649(1996).
DR EMBL; U58031; AAB00320.1; -.
DR EMBL; U57979; AAA99830.1; -.
DR EMBL; U57978; AAA99829.1; -.
DR EMBL; U57762; AAB00317.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1231 MW; 455099E3A87041A7 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 9 Q 9

RESULT 74
Q47451
ID Q47451 PRELIMINARY; PRT; 11 AA.
AC Q47451;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Plasmid pRJ1004 DNA (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=pRJ1004;
RX MEDLINE=96130847; PubMed=8594334;
RA Brown N.L., Barrett S.R., Camakaris J., Lee B.T., Rouch D.A.;
RT "Molecular genetics and transport analysis of the copper-resistance
RT determinants (pco) from Escherichia coli plasmid pRJ1004.";
RL Mol. Microbiol. 17:1153-1166(1995).
DR EMBL; X83541; CAA58524.1; -.
DR PIR; S70166; S52252.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; 47D864F8ADC1A057 CRC64;

Query Match 9.1%; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 N 10
|
Db 2 N 2

RESULT 75
Q9AIZ7
ID Q9AIZ7 PRELIMINARY; PRT; 11 AA.
AC Q9AIZ7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tryptophanyl-tRNA synthetase (Fragment).
GN TRPS.
OS Carsonella ruddii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Carsonella.
OX NCBI_TaxID=114186;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20336438; PubMed=10877784;
RA Thao M.L., Moran N.A., Abbot P., Brennan E.B., Burckhardt D.H.,
RA Baumann P.;
RT "Cosppeciation of psyllids and their primary prokaryotic
RT endosymbionts.";
RL Appl. Environ. Microbiol. 66:2898-2905(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125546; PubMed=11222582;
RA Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
RT "Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
RL J. Bacteriol. 183:1853-1861(2001).
DR EMBL; AF211132; AAK15377.1; -.
DR GO; GO:0004812; F:tRNA ligase activity; IEA.
KW Aminoacyl-tRNA synthetase.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1333 MW; A28C67D6533059C6 CRC64;

Query Match 9.18; Score 1; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 7 K 7

Search completed: April 8, 2004, 15:46:09
Job time : 27.7692 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds
(without alignments)
111.135 Million cell updates/sec

Title: US-09-787-443A-20

Perfect score: 11

Sequence: 1 AKKKEQKQRNA 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	DB	
1	2	18.2	11	1	ASL2_BACSE P83147 bacteroides
2	2	18.2	11	1	CSI5_BACSU P81095 bacillus su
3	2	18.2	11	1	LADD_ONCMY P81018 oncorhynchus
4	2	18.2	11	1	LSK1_LEUMA P04428 leucophaea
5	2	18.2	11	1	LSKP_PERAM P36885 periplaneta
6	2	18.2	11	1	PVK1_PERAM P41837 periplaneta
7	2	18.2	11	1	Q2OA_COMTE P80464 comamonas t
8	2	18.2	11	1	TKC2_CALVO P41518 calliphora
9	2	18.2	11	1	TKN1_UPEIN P82026 uperoleia i
10	2	18.2	11	1	TKN1_UPERU P08612 uperoleia r
11	1	9.1	11	1	ANGT_CRIGE P09037 crinia georgia
12	1	9.1	11	1	ASL1_BACSE P83146 bacteroides
13	1	9.1	11	1	BPP3_BOTIN P30423 bothrops in
14	1	9.1	11	1	BPP4_BOTIN P30424 bothrops in
15	1	9.1	11	1	BPPB_AGKHA P01021 agkistrodon
16	1	9.1	11	1	BPP_AGKHP P04562 agkistrodon
17	1	9.1	11	1	BRK_MEGFL P12797 megascolia

18	1	9.1	11	1	CA21_LITCI	P82087	litoria cit
19	1	9.1	11	1	CA22_LITCI	P82088	litoria cit
20	1	9.1	11	1	CA31_LITCI	P82089	litoria cit
21	1	9.1	11	1	CA32_LITCI	P82090	litoria cit
22	1	9.1	11	1	CA41_LITCI	P82091	litoria cit
23	1	9.1	11	1	CA42_LITCI	P82092	litoria cit
24	1	9.1	11	1	CEP1_ACHFU	P22790	achatina fu
25	1	9.1	11	1	CORZ_PERAM	P11496	periplaneta
26	1	9.1	11	1	COXA_CANFA	P99501	canis famil
27	1	9.1	11	1	CX5A_CONAL	P58848	conus aulic
28	1	9.1	11	1	CX5B_CONAL	P58849	conus aulic
29	1	9.1	11	1	CXL1_CONMR	P58807	conus marmo
30	1	9.1	11	1	EFG_CLOPA	P81350	clostridium
31	1	9.1	11	1	ES1_RAT	P56571	rattus norv
32	1	9.1	11	1	FAR6_PENMO	P83321	penaeus mon
33	1	9.1	11	1	FAR9_CALVO	P41864	calliphora
34	1	9.1	11	1	HS70_PINPS	P81672	pinus pinas
35	1	9.1	11	1	LPW_THETH	P05624	thermus the
36	1	9.1	11	1	MHBI_KLEPN	P80580	klebsiella
37	1	9.1	11	1	MLG_THETS	P41989	theromyzon
38	1	9.1	11	1	MORN_HUMAN	P01163	homo sapien
39	1	9.1	11	1	NUHM_CANFA	P49820	canis famil
40	1	9.1	11	1	NXSN_PSETE	P59072	pseudonaja
41	1	9.1	11	1	OAIF_SARBU	P83518	sarcophaga
42	1	9.1	11	1	PKC1_CARMO	P82684	carausius m
43	1	9.1	11	1	PQQC_PSEFL	P55173	pseudomonas
44	1	9.1	11	1	RANC_RANPI	P08951	rana pipien
45	1	9.1	11	1	RR2_CONAM	P42341	conopholis
46	1	9.1	11	1	RRPL_CHAV	P13179	chandipura
47	1	9.1	11	1	RS30_ONCMY	P83328	oncorhynchu
48	1	9.1	11	1	T2P1_PROVU	P31031	proteus vul
49	1	9.1	11	1	TIN1_HOPTI	P82651	hoplobatrac
50	1	9.1	11	1	TIN4_HOPTI	P82654	hoplobatrac
51	1	9.1	11	1	TKN1_PSEGU	P42986	pseudophryne
52	1	9.1	11	1	TKN2_PSEGU	P42987	pseudophryne
53	1	9.1	11	1	TKN2_UPERU	P08616	uperoleia r
54	1	9.1	11	1	TKN3_PSEGU	P42988	pseudophryne
55	1	9.1	11	1	TKN4_PSEGU	P42989	pseudophryne
56	1	9.1	11	1	TKN5_PSEGU	P42990	pseudophryne
57	1	9.1	11	1	TKNA_CHICK	P19850	gallus gall
58	1	9.1	11	1	TKNA_GADMO	P28498	gadus morhu
59	1	9.1	11	1	TKNA_HORSE	P01290	equus cabal
60	1	9.1	11	1	TKNA_ONCMY	P28499	oncorhynchu
61	1	9.1	11	1	TKNA_RANCA	P22688	rana catesbeiana
62	1	9.1	11	1	TKNA_RANRI	P29207	rana ridibunda
63	1	9.1	11	1	TKNA_SCYCA	P41333	scyliorhinus
64	1	9.1	11	1	TKND_RANCA	P22691	rana catesbeiana
65	1	9.1	11	1	TKN_ELEMO	P01293	eledone moschata
66	1	9.1	11	1	TKN_PHYFU	P08615	physalaemus
67	1	9.1	11	1	UF05_MOUSE	P38643	mus musculus
68	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapien
69	1	9.1	11	1	UXB2_YEAST	P99013	saccharomyces
70	0	0.0	11	1	RE41_LITRU	P82074	litoria rubra

ALIGNMENTS

RESULT 1

ASL2_BACSE

ID ASL2_BACSE STANDARD; PRT; 11 AA.

AC P83147;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).

OS Bacteroides stercoris.

OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;

OC Bacteroidaceae; Bacteroides.

OX NCBI_TaxID=46506;

RN [1]

RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.

RC STRAIN=HJ-15;

RX MEDLINE=21223019; PubMed=11322884;

RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;

RT "Purification and characterization of acharan sulfate lyases, two novel heparinases, from Bacteroides stercoris HJ-15.";

RL Eur. J. Biochem. 268:2635-2641(2001).

CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent, heparin and heparan sulfate.

CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead. Activated by reducing agents, such as DL-dithiothreitol and 2-mercaptoethanol.

CC -!- SUBUNIT: Monomer.

CC -!- PTM: The N-terminus is blocked.

CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is 7.2 and optimum temperature 45 degrees Celsius.

KW Lyase; Heparin-binding.

FT NON_TER 1 1

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QR 9

||

Db 10 QR 11

RESULT 2

CSI5_BACSU

ID CSI5_BACSU STANDARD; PRT; 11 AA.

AC P81095;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

RP SEQUENCE.

RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to Swiss-Prot.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in *Bacillus subtilis*.";
RL *J. Bacteriol.* 178:4611-4619(1996).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: In response to low temperature.
CC -!- CAUTION: Could not be found in the genome of *B. subtilis* 168.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10
||
Db 2 RN 3

RESULT 3
LADD_ONCMY
ID LADD_ONCMY STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS *Oncorhynchus mykiss* (Rainbow trout) (*Salmo gairdneri*).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; *Oncorhynchus*.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jenseunius J.C.;
RT "A rainbow trout lectin with multimeric structure.";
RL *Comp. Biochem. Physiol.* 116B:385-390(1997).
CC -!- FUNCTION: Lectin that binds sepharose.
CC -!- COFACTOR: Calcium is essential for sepharose binding.
CC -!- SUBUNIT: Multimeric.
KW Lectin; Calcium.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10

||
Db 5 RN 6

RESULT 4

LSK1_LEUMA

ID LSK1_LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leucosulfakinin-I (LSK-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC -!- FUNCTION: Change the frequency and amplitude of contractions of
the hingut. Inhibits muscle contraction of hindgut.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A01622; GMROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||
Db 1 EQ 2

RESULT 5

LSKP_PERAM

ID LSKP_PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockroach homologous to the leucosulfakinins.";
RL *Neuropeptides* 14:145-149(1989).
CC -!-- FUNCTION: Stimulates hindgut contractions.
CC -!-- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EQ 6
||
Db 1 EQ 2

RESULT 6
PVK1_PERAM
ID PVK1_PERAM STANDARD PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisynthetic organs;
RX MEDLINE=95232021; PubMed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the perisynthetic organs of the American cockroach.";
RL *Peptides* 16:61-66(1995).
CC -!-- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RN 10
||
Db 10 RN 11

RESULT 7

Q2OA_COMTE

ID Q2OA_COMTE STANDARD; PRT; 11 AA.
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: Converts (3-methyl)-quinoline to (3-methyl)-2-oxo-1,2-dihydroquinoline.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl)-quinoline; first step.
CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and two gamma chains (Probable).
DR PIR; S66606; S66606.
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 8

TKC2_CALVO

ID TKC2_CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: Myoactive peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 5 NA 6

RESULT 9
TKN1_UPEIN
ID TKN1_UPEIN STANDARD; PRT; 11 AA.
AC P82026;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperin 1.1.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.

CC --!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC --!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
 CC --!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 10 NA 11
 ||
 Db 5 NA 6

RESULT 10
 TKN1_UPERU
 ID TKN1_UPERU STANDARD; PRT; 11 AA.
 AC P08612;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperolein.
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspamer V., Endean R.;
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
 in the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC --!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC --!- SUBCELLULAR LOCATION: Secreted.
 CC --!- TISSUE SPECIFICITY: Skin.
 CC --!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NA 11
||
Db 5 NA 6

RESULT 11
ANGT_CRIGE
ID ANGT_CRIGE STANDARD; PRT; 11 AA.
AC P09037;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Crinia-angiotensin II.
OS Crinia georgiana (Quacking frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Crinia.
OX NCBI_TaxID=8374;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80024575; PubMed=488254;
RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
RT "Amino acid composition and sequence of crinia-angiotensin, an
RT angiotensin II-like endecapeptide from the skin of the Australian
RT frog Crinia georgiana.";
RL Experientia 35:1132-1133(1979).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S07207; S07207.
KW Vasoconstrictor.
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 A 1
|
Db 1 A 1

RESULT 12
ASL1_BACSE
ID ASL1_BACSE STANDARD; PRT; 11 AA.
AC P83146;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).

OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.";
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 11 Q 11

RESULT 13
BPP3_BOTIN
ID BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 14
BPP4_BOTIN
ID BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; D37196; D37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 15

BPPB_AGKHA

ID BPPB_AGKHA STANDARD; PRT; 11 AA.

AC P01021;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide B (Angiotensin-converting enzyme inhibitor).

OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Gloydius.

OX NCBI_TaxID=242054;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RA Kato H., Suzuki T.;

RT "Amino acid sequence of bradykinin-potentiating peptide isolated from the venom of Agkistrodon halys blomhoffii.";

RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).

CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.

DR PIR; A01254; XASNBA.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6

 |

Db 1 Q 1

RESULT 16

BPP_AGKHP

ID BPP_AGKHP STANDARD; PRT; 11 AA.

AC P04562;

DT 13-AUG-1987 (Rel. 05, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).

OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydius halys pallas).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Gloydius.

OX NCBI_TaxID=8714;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;
 RX MEDLINE=86177022; PubMed=3008123;
 RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
 RT "Structure-function studies on the bradykinin potentiating peptide
 from Chinese snake venom (Agkistrodon halys pallasi).";
 RL Peptides 6 Suppl. 3:339-342(1985).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; JC0002; XAVIBH.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 6 Q 6
 |
 Db 1 Q 1

RESULT 17
 BRK_MEGFL
 ID BRK_MEGFL STANDARD; PRT; 11 AA.
 AC P12797;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
 peptide ([Thr6]bradykinin)].
 OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Scoliidae; Megascolia.
 OX NCBI_TaxID=7437;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 RT solitary wasp Megascolia flavifrons.";
 RL Toxicon 25:527-535(1987).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Nakajima T., Piek T., Yashuara T., Mantel P.;
 RT "Two kinins isolated from the venom of Megascolia flavifrons.";
 RL Toxicon 26:34-34(1988).
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 DR PIR; B26744; B26744.

DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 1 R 1

RESULT 18
CA21_LITCI
ID CA21_LITCI STANDARD; PRT; 11 AA.
AC P82087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 2.1/2.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 Q 6
|
Db 1 Q 1

RESULT 19

CA22_LITCI

ID CA22_LITCI STANDARD; PRT; 11 AA.
AC P82088;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 2.2/2.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 Q 6
|
Db 1 Q 1

RESULT 20

CA31_LITCI

ID CA31_LITCI STANDARD; PRT; 11 AA.

AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!-- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!-- SUBCELLULAR LOCATION: Secreted.
 CC -!-- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!-- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 CC sulfated.
 CC -!-- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -!-- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 21
 CA32_LITCI
 ID CA32_LITCI STANDARD; PRT; 11 AA.
 AC P82090;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.2/3.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;

RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 22
CA41_LITCI
ID CA41_LITCI STANDARD; PRT; 11 AA.
AC P82091;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 4.1/4.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 23
 CA42_LITCI
 ID CA42_LITCI STANDARD; PRT; 11 AA.
 AC P82092;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.2/4.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being sulfated.
 CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 24
CEP1_ACHFU
ID CEP1_ACHFU STANDARD; PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmuerehra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also
CC excitatory actions on the penis retractor muscle, the buccal
CC muscle and the identified neurons controlling the buccal muscle
CC movement of achatina.
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 3 Q 3

RESULT 25
CORZ_PERAM
ID CORZ_PERAM STANDARD; PRT; 11 AA.
AC P11496;

DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Corazonin.
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132;
 RA Veenstra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from
 the American cockroach.";
 RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
 in the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 26
 COXA_CANFA
 ID COXA_CANFA STANDARD; PRT; 11 AA.
 AC P99501;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
 GN COX5A.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c

CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O₂ = 4 ferricyanochrome
CC c + 2 H₂O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
DR HSC-2DPAGE; P99501; DOG.
DR InterPro; IPR003204; Cyt_c_ox5A.
DR Pfam; PF02284; COX5A; 1.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 E 5
|
Db 6 E 6

RESULT 27

CX5A_CONAL

ID CX5A_CONAL STANDARD; PRT; 11 AA.
AC P58848;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5a.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins.";
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
CC observed when injected into mice.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
DR PIR; A59146; A59146.
KW Toxin.

FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 7 R 7

RESULT 28

CX5B_CONAL

ID CX5B_CONAL STANDARD; PRT; 11 AA.
AC P58849;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5b.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99452958; PubMed=10521453;
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RT "The T-superfamily of conotoxins.";
RL J. Biol. Chem. 274:30664-30671(1999).
RN [2]
RP ERRATUM.
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
RL J. Biol. Chem. 274:36030-36030(1999).
CC --!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
CC observed when injected into mice (By similarity).
CC --!- SUBCELLULAR LOCATION: Secreted.
CC --!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC --!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.
CC --!- SIMILARITY: Belongs to the conotoxin T-superfamily.
DR PIR; B59146; B59146.
KW Toxin.
FT DISULFID 2 9
FT DISULFID 3 10
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 7 R 7

RESULT 29

CXL1_CONMR

ID CXL1_CONMR STANDARD; PRT; 11 AA.
AC P58807;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda-conotoxin CMrVIA.
OS Conus marmoreus (Marble cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=42752;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20564325; PubMed=10988292;
RA Balaji R.A., Otake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA Seow K.T., Bay B.-H.;
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
RT pattern and protein folding. Isolation and characterization from the
RT venom of Conus marmoreus.";
RL J. Biol. Chem. 275:39516-39522(2000).
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
KW Neurotoxin; Toxin; Hydroxylation.
FT DISULFID 2 11
FT DISULFID 3 8
FT MOD_RES 10 10 HYDROXYLATION.
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 6 K 6

RESULT 30

EFG_CLOPA

ID EFG_CLOPA STANDARD; PRT; 11 AA.
AC P81350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (CP 5) (Fragment).
GN FUSA.

OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC --!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC --!- SUBCELLULAR LOCATION: Cytoplasmic.
CC --!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.
DR InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 31
ES1_RAT
ID ES1_RAT STANDARD PRT; 11 AA.
AC P56571;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE ES1 protein, mitochondrial (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC --!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC --!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot
CC P2) is: 8.9, its MW is: 25 kDa.
CC --!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
KW Mitochondrion.
FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;
Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 1 R 1

RESULT 32
FAR6_PENMO
ID FAR6_PENMO STANDARD; PRT; 11 AA.
AC P83321;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC --!- SUBCELLULAR LOCATION: Secreted.
CC --!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
CC --!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 3 R 3

RESULT 33
FAR9_CALVO
ID FAR9_CALVO STANDARD; PRT; 11 AA.
AC P41864;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 9.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; I41978; I41978.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 5 K 5

RESULT 34
HS70_PINPS
ID HS70_PINPS STANDARD; PRT; 11 AA.
AC P81672;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Heat shock 70 kDa protein (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N164) is: 5.4, its MW is: 73 kDa.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

KW ATP-binding; Heat shock; Multigene family.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 E 5
|
Db 2 E 2

RESULT 35
LPW_THETH
ID LPW_THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT HB8 trpE and trpG.";
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X07744; CAA30565.1; -.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 2 A 2

RESULT 36

MHBI_KLEPN

ID MHBI_KLEPN STANDARD; PRT; 11 AA.
 AC P80580;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
 GN MHBI.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96349117; PubMed=8760924;
 RA Robson N.D., Parrott S., Cooper R.A.;
 RT "In vitro formation of a catabolic plasmid carrying Klebsiella pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-hydroxybenzoate.";
 RL Microbiology 142:2115-2120(1996).
 CC --!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
 KW Isomerase.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 K 2
 |
 Db 2 K 2

RESULT 37

MLG_THETS

ID MLG_THETS STANDARD; PRT; 11 AA.
 AC P41989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 OX NCBI_TaxID=13286;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94298944; PubMed=8026574;
 RA Salzet M., Wattez C., Bulet P., Malecha J.;
 RT "Isolation and structural characterization of a novel peptide related to gamma-melanocyte stimulating hormone from the brain of the leech Theromyzon tessulatum.";

RL FEBS Lett. 348:102-106(1994).
CC -!- SIMILARITY: Belongs to the POMC family.
DR PIR; S45698; S45698.
KW Hormone; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 10 K 10

RESULT 38
MORN_HUMAN
ID MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuropeptide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;

RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
CC in the G2/mitosis transition.
CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
CC and was called head activator by the authors, because it induced
CC head-specific growth and differentiation in this animal. It has
CC been found in mammalian intestine and hypothalamus.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHXAE.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 39
NUHM_CANFA
ID NUHM_CANFA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC FRAGMENT OF THE ENZYME.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).

CC --!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
 CC --!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
 CC mitochondrial inner membrane.
 CC --!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
 DR HSC-2DPAGE; P49820; DOG.
 DR InterPro; IPR002023; Cmplx1_24kDa.
 DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
 KW Iron-sulfur; Iron; 2Fe-2S.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 A 1
 |
 Db 2 A 2

RESULT 40
 NXSN_PSETE
 ID NXSN_PSETE STANDARD; PRT; 11 AA.
 AC P59072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).
 OS Pseudonaja textilis (Eastern brown snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99449602; PubMed=10518793;
 RA Gong N.L., Armugam A., Jeyaseelan K.;
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
 cloning, expression and protein characterization.";
 RL Eur. J. Biochem. 265:982-989(1999).
 CC --!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
 CC acetylcholine receptors (nAChR).
 CC --!- SUBCELLULAR LOCATION: Secreted.
 CC --!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC --!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
 CC --!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
 CC --!- SIMILARITY: Belongs to the snake toxin family.
 DR InterPro; IPR003571; Snake_toxin.
 DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
 KW Acetylcholine receptor inhibitor; Multigene family.
 FT UNSURE 3 3
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 5 K 5

RESULT 41

OAIF_SARBU
ID OAIF_SARBU STANDARD; PRT; 11 AA.
AC P83518;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-
DE ODAIF(1-9); Neb-ODAIF(1-7)].
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE=Ovary;
RX MEDLINE=22272747; PubMed=12383874;
RA Vandingen A., Hens K., Baggerman G., Macours N., Schoofs L.,
RA De Loof A., Huybrechts R.;
RT "Isolation and characterization of an angiotensin converting enzyme
RT substrate from vitellogenetic ovaries of Neobellieria bullata.";
RL Peptides 23:1853-1863(2002).
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
CC vitro.
CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-
CC terminal dipeptides.
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
FT PEPTIDE 1 11 NEB-ODAIF.
FT PEPTIDE 1 9 NEB-ODAIF(1-9).
FT PEPTIDE 1 7 NEB-ODAIF(1-7).
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 N 10
|
Db 1 N 1

RESULT 42

PKC1_CARMO
ID PKC1_CARMO STANDARD; PRT; 11 AA.
AC P82684;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).
OS Carausius morosus (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
OC Heteronemiidae; Carausius.
OX NCBI_TaxID=7022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RA Predel R., Kellner R., Gaede G.;
RT "Myotropic neuropeptides from the retrocerebral complex of the stick
insect, Carausius morosus (Phasmatodea: Lonchodidae).";
RL Eur. J. Entomol. 96:275-278(1999).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 E 5
|
Db 2 E 2

RESULT 43
PQQC_PSEFL
ID PQQC_PSEFL STANDARD; PRT; 11 AA.
AC P55173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone
DE biosynthesis protein C) (Fragment).
GN PQQC.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHA0;
RX MEDLINE=96064397; PubMed=8526497;
RA Schnider U., Keel C., Defago G., Haas D.;
RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:
RT mutational inactivation of the genes results in overproduction of the
RT antibiotic pyoluteorin.";
RL Appl. Environ. Microbiol. 61:3856-3864(1995).

CC --!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC --!- SIMILARITY: Belongs to the pqqC family.
CC -----
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CC -----
DR EMBL; X87299; CAA60734.1; -.
DR PIR; S58244; S58244.
DR HAMAP; MF_00654; -; 1.
KW PQQ biosynthesis.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 8 A 8

RESULT 44
RANC_RANPI
ID RANC_RANPI STANDARD; PRT; 11 AA.
AC P08951;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatensin-C.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;
RA Nakajima T.;
RL Unpublished results, cited by:
RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC --!- SUBCELLULAR LOCATION: Secreted.
CC --!- TISSUE SPECIFICITY: Skin.
CC --!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
CC family.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 4 Q 4

RESULT 45

RR2_CONAM

ID RR2_CONAM STANDARD; PRT; 11 AA.
AC P42341;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S2 (Fragment).
GN RPS2.
OS Conopholis americana (Squawroot).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids;
OC lamiids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.
OX NCBI_TaxID=4179;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92145776; PubMed=1723664;
RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
of photosynthesis in a lineage of parasitic plants.";
RL Curr. Genet. 20:515-518(1991).
CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC -----
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CC -----
DR EMBL; X64567; CAA45868.1; -.
DR PIR; S32575; S32575.
DR HAMAP; MF_00291; -; 1.
DR InterPro; IPR001865; Ribosomal_S2.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Ribosomal protein; Chloroplast.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 E 5

Db 11 E 11

RESULT 46
RRPL CHAV

ID RRPL CHAV STANDARD; PRT; 11 AA.
AC P13179;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein) (Fragment).
GN L.
OS Chandipura virus (strain I653514).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11273;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89299473; PubMed=2741347;
RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
RA Banerjee A.K.;
RT "Structure and expression of the glycoprotein gene of Chandipura
RT virus.";
RL Virology 171:285-290(1989).
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
CC NUCLEOCAPSID (N) PROTEIN.
CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RABDOVIRUSES AND
CC PARAMYXOVIRUSES.
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CC -----
DR EMBL; J04350; AAA42917.1; -.
KW Transferase; RNA-directed RNA polymerase.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 N 10
|
Db 4 N 4

RESULT 47

RS30_ONCMY

ID RS30_ONCMY STANDARD; PRT; 11 AA.

AC P83328;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 40S ribosomal protein S30 (Fragment).

GN FAU.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Skin mucus;

RX MEDLINE=22142142; PubMed=12147245;

RA Fernandes J.M.O., Smith V.J.;

RT "A novel antimicrobial function for a ribosomal peptide from rainbow trout skin.";

RL Biochem. Biophys. Res. Commun. 296:167-171(2002).

CC -!- FUNCTION: Has antibacterial activity against Gram-positive bacteria.

CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.

CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.

KW Ribosomal protein; Antibiotic.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2

 |

Db 1 K 1

RESULT 48

T2P1_PROVU

ID T2P1_PROVU STANDARD; PRT; 11 AA.

AC P31031;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)

DE (R.PvuI) (Fragment).

GN PVUIR.

OS Proteus vulgaris.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Proteus.

OX NCBI_TaxID=585;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 13315;

RX MEDLINE=93087186; PubMed=1454536;
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuI restriction and
RT modification system.";
RL Nucleic Acids Res. 20:5743-5747(1992).
CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC CLEAVES AFTER T-4.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L04163; AAA25660.1; -.
DR PIR; S35490; S35490.
DR REBASE; 1541; PvuI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 E 5
|
Db 5 E 5

RESULT 49
TIN1_HOPTI
ID TIN1_HOPTI STANDARD; PRT; 11 AA.
AC P82651;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tigerinin-1.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,

CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
FT DISULFID 2 10
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 9 R 9

RESULT 50
TIN4_HOPTI
ID TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tigerinin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaran N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 1 R 1

RESULT 51

TKN1_PSEGU

ID TKN1_PSEGU STANDARD; PRT; 11 AA.

AC P42986;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Kassinin-like peptide K-I (PG-KI).

OS Pseudophryne guentheri (Guenther's toadlet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Myobatrachinae; Pseudophryne.

OX NCBI_TaxID=30349;

RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RX MEDLINE=90287814; PubMed=2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guntheri.";

RL Peptides 11:299-304(1990).

CC -!- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretagogues, and contract (directly or indirectly) many smooth muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; B60409; B60409.

DR InterPro; IPR002040; Tachy_Neurokinin.

DR InterPro; IPR008215; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.

DR PROSITE; PS00267; TACHYKININ; 1.

KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 9e+04;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 Q 6
|
Db 1 Q 1

RESULT 52

TKN2_PSEGU

ID TKN2_PSEGU STANDARD; PRT; 11 AA.

AC P42987;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-II (PG-KII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; C60409; C60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 53
 TKN2_UPERU
 ID TKN2_UPERU STANDARD; PRT; 11 AA.
 AC P08616;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80223080; PubMed=7389029;
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
 RT "Physalaemin- and bombesin-like peptides in the skin of the
 Australian leptodactylid frog *Uperoleia rugosa*.";
 RL Chem. Pharm. Bull. 28:689-695(1980).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 evoke behavioral responses, are potent vasodilators and
 secretagogues, and contract (directly or indirectly) many smooth
 muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 54
 TKN3_PSEGU
 ID TKN3_PSEGU STANDARD; PRT; 11 AA.
 AC P42988;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-III (PG-KIII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog *Pseudophryne guntheri*.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 evoke behavioral responses, are potent vasodilators and

CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D60409; D60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 55
 TKN4_PSEGU
 ID TKN4_PSEGU STANDARD; PRT; 11 AA.
 AC P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P-like peptide I (PG-SPI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; E60409; E60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.

DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

 Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 Q 6
 |
 Db 1 Q 1

RESULT 56
 TKN5_PSEGU
 ID TKN5_PSEGU STANDARD; PRT; 11 AA.
 AC P42990;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P-like peptide II (PG-SPII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; F60409; F60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;
Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 57
TKNA_CHICK
ID TKNA_CHICK STANDARD; PRT; 11 AA.
AC P19850;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=88204263; PubMed=2452461;
RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
RL Regul. Pept. 20:171-180(1988).
CC --!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC --!- SUBCELLULAR LOCATION: Secreted.
CC --!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; JN0023; JN0023.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
|
Db 1 R 1

RESULT 58
TKNA_GADMO

ID TKNA_GADMO STANDARD; PRT; 11 AA.
AC P28498;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS *Gadus morhua* (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; *Gadus*.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S23306; S23306.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 59
TKNA_HORSE
ID TKNA_HORSE STANDARD; PRT; 11 AA.
AC P01290;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
GN TAC1 OR NKNA OR TAC2 OR NKA.
OS *Equus caballus* (Horse), and
OS *Cavia porcellus* (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; *Equus*.

OX NCBI_TaxID=9796, 10141;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Horse;
 RA Studer R.O., Trzeciak A., Lergier W.;
 RT "Isolation and amino-acid sequence of substance P from horse
 intestine.";
 RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.porcellus;
 RX MEDLINE=90044685; PubMed=2478925;
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P.";
 RL Neuropeptides 14:105-110(1989).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01558; SPHO.
 DR PIR; A60654; A60654.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 R 9
 |
 Db 1 R 1

RESULT 60
 TKNA_ONCMY
 ID TKNA_ONCMY STANDARD; PRT; 11 AA.
 AC P28499;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;

RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout.";
RL Eur. J. Biochem. 206:659-664(1992).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S23308; S23308.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 61
TKNA_RANCA
ID TKNA_RANCA STANDARD; PRT; 11 AA.
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin A (RTK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";

RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A61033; A61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2 K 2
Db	1 K 1

RESULT 62
 TKNA_RANRI
 ID TKNA_RANRI STANDARD; PRT; 11 AA.
 AC P29207;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranakinin (Substance-P-related peptide).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92044543; PubMed=1658233;
 RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
 RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
 RT neurokinin B from the brain of the frog Rana ridibunda.";
 RL J. Neurochem. 57:2086-2091(1991).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.

KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 63

TKNA_SCYCA
ID TKNA_SCYCA STANDARD; PRT; 11 AA.
AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyliorhinus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -!-- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!-- SUBCELLULAR LOCATION: Secreted.
CC -!-- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S33300; S33300.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 64

TKND_RANCA

ID TKND_RANCA STANDARD; PRT; 11 AA.

AC P22691;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ranatachtykinin D (RTK D).

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Intestine;

RX MEDLINE=91254337; PubMed=2043143;

RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;

RT "Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.";

RL Biochem. Biophys. Res. Commun. 177:588-595(1991).

RN [2]

RP SEQUENCE.

RC TISSUE=Intestine;

RX MEDLINE=94023216; PubMed=8210506;

RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;

RT "Four novel tachykinins in frog (Rana catesbeiana) brain and intestine.";

RL Regul. Pept. 46:81-88(1993).

CC -- FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasodilators and secretagogues, and contract (directly or indirectly) many smooth muscles.

CC -- SUBCELLULAR LOCATION: Secreted.

CC -- SIMILARITY: Belongs to the tachykinin family.

DR PIR; D61033; D61033.

DR InterPro; IPR002040; Tachy_Neurokinin.

DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.

KW Tachykinin; Neuropeptide; Amidation.

FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 1 K 1

RESULT 65

TKN_ELEMO

ID TKN_ELEMO STANDARD; PRT; 11 AA.

AC P01293;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Eledoisin.

OS Eledone moschata (Musky octopus) (Ozaena moschata), and
OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
OX NCBI_TaxID=6641, 102876;
RN [1]
RP SEQUENCE.
RA Anastasi A., Erspamer V.;
RT "The isolation and amino acid sequence of eleodoisin, the active
RT endecapeptide of the posterior salivary glands of Eledone.";
RL Arch. Biochem. Biophys. 101:56-65(1963).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A01561; EOCO.
DR PIR; B01561; EOOC.
DR PDB; 1MXQ; 18-FEB-03.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
KW 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 66
TKN_PHYFU
ID TKN_PHYFU STANDARD; PRT; 11 AA.
AC P08615;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Physalaemin.
OS Physalaemus fuscumaculatus (Neotropical frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Leptodactylinae; Physalaemus.
OX NCBI_TaxID=8378;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=66076612; PubMed=5857249;
RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
RT "Structure and pharmacological actions of physalaemin, the main

RT active polypeptide of the skin of *Physalaemus fuscumaculatus*.";
RL *Experientia* 20:489-490(1964).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S07201; S07201.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 1 Q 1

RESULT 67
UF05_MOUSE
ID UF05_MOUSE STANDARD; PRT; 11 AA.
AC P38643;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).
OS *Mus musculus* (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Mus*.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 48 kDa.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
|
Db 1 K 1

RESULT 68
ULAG_HUMAN
ID ULAG_HUMAN STANDARD; PRT; 11 AA.
AC P31933;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993.";
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 34 kDa.
DR SWISS-2DPAGE; P31933; HUMAN.
DR Siena-2DPAGE; P31933; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 Q 6
|
Db 3 Q 3

RESULT 69
UXB2_YEAST
ID UXB2_YEAST STANDARD; PRT; 11 AA.
AC P99013;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RC STRAIN=X2180-1A;
RA Sanchez J.-C., Golaz O., Schaller D., Morsch F., Frutiger S.,

RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
RL Submitted (AUG-1995) to Swiss-Prot.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.20, its MW is: 9.2 kDa.
DR SWISS-2DPAGE; P99013; YEAST.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 7 A 7

RESULT 70
RE41_LITRU
ID RE41_LITRU STANDARD; PRT; 11 AA.
AC P82074;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 0.0%; Score 0; DB 1; Length 11;
Best Local Similarity 0.0%; Pred. No. 1.4e+05;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 1 G 1

Search completed: April 8, 2004, 15:47:23
Job time : 5.15385 secs